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OM protein - protein search, using sw model

Run on: December 3, 2005, 23:22:13 ; Search time 186 Seconds
(without alignments)
18.898 Million cell updates/sec

Title: US-10-807-553-2

Perfect score: 48

Sequence: 1 HDAPIGYD 8

Scoring table: BIOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 100 summaries

Database :
1: A_Geneseq_21:*
2: geneseqp1980s:*
3: geneseqp1990s:*
4: geneseqp2000s:*
5: geneseqp2001s:*
6: geneseqp2002s:*
7: geneseqp2003as:*
8: geneseqp2004s:*
9: geneseqp2005s:*
Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	48	100.0	8	2	AAW54884 Isozyme-B
2	48	100.0	8	6	ABB99501 Amino aci
3	48	100.0	8	6	ABG76120 Psilepsillo
4	48	100.0	8	9	AEA89881 Receptor
5	48	100.0	30	9	AEA89971 Receptor
6	48	100.0	737	5	AAO18490 Human ins
7	48	100.0	737	6	ADA50073 Mouse pro
8	48	100.0	737	6	AAE39167 Mouse pro
9	48	100.0	737	7	ADE57469 Human pro
10	48	100.0	737	7	ADE57441 Human pro
11	48	100.0	737	7	ADE58354 Human pro
12	48	100.0	737	7	ADE57531 Rat prote
13	48	100.0	737	7	ADE57533 Human pro
14	48	100.0	737	7	ADE58352 Rat prote
15	48	100.0	737	7	ADE57535 Rat prote
16	48	100.0	737	7	ADE57537 Rat prote
17	48	100.0	737	7	ADE57539 Rat prote
18	48	100.0	737	7	ADE57527 Human pro
19	48	100.0	737	7	ADE57529 Human pro
20	48	100.0	737	9	ADY80150 Amino aci
21	48	100.0	737	9	ADY80138 Amino aci
22	48	100.0	737	9	ADY80140 Amino aci
23	48	100.0	737	9	ADY80151 Amino aci
24	44	91.7	8	6	ABB99506 Amino aci

25	44	91.7	8	6	ABB99512 Amino aci
26	44	91.7	8	6	ABG76125 Psilepsillo
27	44	91.7	8	6	ABG76131 Psilepsillo
28	44	91.7	8	9	AEA89893 Receptor
29	44	91.7	8	9	AEA89887 Receptor
30	44	91.7	8	9	AEA89909 Receptor
31	43	89.6	8	2	AAW54889 Isozyme-B
32	43	89.6	8	2	AAW54892 Isozyme-B
33	43	89.6	8	6	ABB99507 Amino aci
34	43	89.6	8	6	ABG76126 Psilepsillo
35	43	89.6	8	6	ABB99513 Receptor
36	43	89.6	8	9	AEA89888 Receptor
37	42	87.5	8	2	AAW54894 Isozyme-B
38	42	87.5	8	2	AAW54895 Isozyme-B
39	42	87.5	8	6	ABB99508 Amino aci
40	42	87.5	8	6	ABG76127 Psilepsillo
41	42	87.5	8	9	AEA89907 Receptor
42	42	87.5	8	9	AEA89889 Receptor
43	42	87.5	11	2	AAW17460 Protein k
44	42	87.5	11	9	ADY80144 Peptide a
45	40	83.3	8	2	AAW54890 Isozyme-B
46	40	83.3	8	2	AAW54891 Isozyme-B
47	40	83.3	8	2	AAW54887 Isozyme-B
48	40	83.3	8	2	AAW54888 Isozyme-B
49	40	83.3	8	6	ABB99511 Amino aci
50	40	83.3	8	6	ABB99513 Amino aci
51	40	83.3	8	6	ABG76130 Psilepsillo
52	40	83.3	8	6	ABG76132 Psilepsillo
53	40	83.3	8	9	AEA89892 Receptor
54	40	83.3	8	9	AEA89957 Receptor
55	40	83.3	8	9	AEA89894 Receptor
56	40	83.3	8	9	AEA89899 Receptor
57	39	81.2	8	2	AAW54893 Isozyme-B
58	38	79.2	8	2	AAW54898 Isozyme-B
59	38	79.2	8	9	AEA89884 Receptor
60	38	79.2	18	9	AEA89974 Receptor
61	38	79.2	35	6	ABR8412 Tumour ce
62	38	79.2	35	7	ADC84758 MCF-7 bre
63	38	79.2	682	5	AAO18491 Human ins
64	38	79.2	682	8	ADM41441 Human pro
65	38	79.2	683	7	ADC37371 Nucleat f
66	38	79.2	683	8	ADJ96615 Human pro
67	38	79.2	683	8	ADM41445 Human pro
68	38	79.2	683	8	ADM41451 Human pro
69	38	79.2	683	8	ADQ96474 T cell ac
70	38	79.2	683	8	ADQ97369 Human can
71	38	79.2	683	9	ADY15668 PRO polyp
72	38	79.2	683	9	AEC01607 Human pro
73	38	79.2	702	8	ADO97364 Mouse can
74	38	79.2	715	8	ADM41450 His-tagge
75	38	79.2	918	8	ADM41449 Glutathio
76	37.5	78.1	14	2	AAW54901 Isozyme-B
77	37	77.1	8	9	AEA89945 Receptor
78	37	77.1	2203	8	ADE62194 Rat prote
79	37	77.1	2203	7	ADD46697 Rat prote
80	37	77.1	2203	7	ADE62198 Rat prote
81	36	75.0	8	6	ABB99516 Amino aci
82	36	75.0	8	6	ABB99505 Amino aci
83	36	75.0	8	6	ABG76135 Psilepsillo
84	36	75.0	8	6	ABG76124 Psilepsillo
85	36	75.0	8	9	AEA89897 Receptor
86	36	75.0	8	9	AEA89886 Receptor
87	36	75.0	8	9	AEA89944 Receptor
88	36	75.0	8	2	AAW54886 Isozyme-B
89	35	72.9	6	2	AAW54888 Isozyme-B
90	35	72.9	6	2	AAW54885 Isozyme-B
91	35	72.9	8	6	ABB99509 Amino aci
92	35	72.9	8	6	ABB99510 Amino aci
93	35	72.9	8	6	ABG76129 Psilepsillo
94	35	72.9	8	6	ABG76128 Psilepsillo
95	35	72.9	8	9	AEA89890 Receptor
96	35	72.9	8	9	AEA89910 Receptor
97	35	72.9	8	9	AEA89935 Receptor

98 35 72.9 8 9 AEA89891
99 35 72.9 8 9 AEA89934
100 35 72.9 8 9 AEA89929

ALIGNMENTS

RESULT 1

AAW54884 ID AAW54884 standard; peptide; 8 AA.

AC AAW54884;

DT 24-SEP-1998 (first entry)

DE Isozyme-specific agonist peptide epsilon VI-7;E7.

KM epsilon-protein kinase C; ischaemic injury; hypoxic exposure.

OS Synthetic.

PM MO981729-A1.

PD 30-APR-1998.

PF 18-OCT-1997 97WO-US018716.

PR 18-OCT-1996; 96US-0028724P.

PA (STRD) UNIV LELAND STANFORD JUNIOR.

PI Mochly-Rosen D;

DR WPI, 1998-261181/23.

PT Peptide agonists of protein kinase C - used to reduce ischaemic injury of

PT cells exposed to hypoxic conditions.

PS Claim 1; Page 32; 47pp; English.

CC The peptides AAW54879-W54901 are agonists of epsilon protein kinase C (PKC). They can be used for reducing ischaemic injury to a cell exposed to hypoxic conditions. They can also be used in a method for identifying a compound effective to induce preconditioning. The peptides are administered at a dose of 1-100 microgram administered once to several times daily in bolus injections

CC Sequence 8 AA;

Query Match 100.0%; Score 48; DB 2; Length 8;

Best Local Similarity 100.0%; Pred. No. 2e+06;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 HDAPIGYD 8

DB 1 HDAPIGYD 8

RESULT 2

ABB99501 ID ABB99501 standard; peptide; 8 AA.

AC ABB99501;

DT 03-MAR-2003 (first entry)

DE Amino acid sequence of a pseudo-epsilon RACK peptide.

KM Pseudo-epsilon RACK; RACK; receptor for activated C-kinase;

KW protein kinase C; PKC; tissue damage; ischaemia; hypoxia.

OS Synthetic.

XX MO200278600-A2.

PN 10-OCT-2002

PF 09-NOV-2001; 2001WO-US051600.

PR 10-NOV-2000; 2000US-0247830P.

PA (STRD) UNIV LELAND STANFORD JUNIOR.

PI Mochly-Rosen D;

DR WPI; 2003-092868/08.

DE New composition comprising pseudo-epsilonRACK peptides, useful for

PT treating tissue damage due to ischemia or hypoxia.

PS Claim 6; Page 27; 30pp; English.

CC The present sequence represents a pseudo-epsilon RACK octapeptide. RACKs (receptors for activated C-kinase) are anchoring molecules, which selectively anchor activated protein kinase C (PKC) isozymes to their respective subcellular sites. Compositions comprising pseudo-epsilon RACK peptides are useful for reducing injury to a cell or tissue exposed to an ischaemic or hypoxic condition. The composition is useful for treating tissue damage due to ischaemia or hypoxia

CC Sequence 8 AA;

Query Match 100.0%; Score 48; DB 6; Length 8;

Best Local Similarity 100.0%; Pred. No. 2e+06;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 HDAPIGYD 8

DB 1 HDAPIGYD 8

RESULT 3

ABG76120 ID ABG76120 standard; peptide; 8 AA.

AC ABG76120;

DT 07-MAY-2003 (first entry)

DE Psepsilon RACK peptide.

KM Epsilon protein kinase C; epsilonPKC; RACK; ischaemia; hypoxia;

KW receptor for activated C-kinase; myocardial infarction;

KM cardiac ischaemia; psepsilon RACK.

OS Synthetic.

PN US2002168354-A1.

PD 14-NOV-2002.

PF 09-NOV-2001; 2001US-00007363.

PR 10-NOV-2000; 2000US-0247830P.

PA (MOCH/) MOCHLY-ROSEN D.

PI Mochly-Rosen D;

DR WPI; 2003-092868/08.

DE New composition comprising pseudo-epsilonRACK peptides, useful for

PT treating tissue damage due to ischemia or hypoxia.

PS Claim 7; Page 8; 17pp; English.

XX The invention relates to reducing injury to a cell or tissue exposed to
CC an ischaemic or hypoxic condition, comprising administering to the cell
CC or tissue a peptide or hypoxic condition, comprising administering to the cell
CC or tissue a peptide or hypoxic condition, comprising administering to the cell
CC The RACK peptide is an agonist of epsilon protein kinase C (epsilonPKC).
CC The method is useful in treating or protecting cells and tissues from
CC damage due to an ischaemic or hypoxic event, such as in cardiac ischaemia
CC or myocardial infarction. The present sequence is the peptide RACK
CC peptide of the invention
XX
SQ Sequence 8 AA;
Query Match 100.0%; Score 48; DB 6; Length 8;
Best Local Similarity 100.0%; Pred. No. 2e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 HDAPICGD 8
Db 1 HDAPICGD 8
RESULT 4
AEA89881
ID AEA89881 standard; peptide, 8 AA.
AC AEA89881;
XX 08-SEP-2005 (first entry)
XX Receptor for activated C kinase (RACK) peptide #3.
XX
XX Protein interaction; protein kinase C; epsilon-PKC; scleroderma;
KM fibrosis; pulmonary fibrosis; septic shock; ischemia;
KM inflammatory bowel disease; autoimmune disease; multiple sclerosis;
KM Guillain Barre syndrome; psoriasis; Graves disease; rheumatoid arthritis;
KM diabetes mellitus; pulmonary disease;
KM chronic obstructive pulmonary disease; asthma;
KM receptor for activated C kinase; RACK; anti-inflammatory; dermatological;
KM hepatotropic; respiratory-gen.; immunosuppressive; neuroprotective;
KM antiproliferative; CNS-gen.; antithyroid; antidiabetic; antirheumatic;
KM antidiabetic; antidiabetic; gastrointestinal-gen.; antibacterial;
KM vasotropic; cardiant.
OS Homo sapiens.
XX
XX WO2005059124-A2.
XX
XX 30-JUN-2005.
XX
XX 13-DEC-2004; 2004WO-US041854.
XX
XX 11-DEC-2003; 2003US-0529223P.
XX
XX (STRD) UNIV LELAND STANFORD JUNIOR.
XX
XX Mochly-Rosen D, Chen LE;
XX
XX WPI; 2005-479333/48.
XX
XX Converting protein kinase C (PKC) agonist peptide to PKC antagonist
XX peptide useful for treating fibrotic or inflammatory disease, involves
XX substituting charged amino acid in agonist peptide with another uncharged
XX amino acid.
XX
XX Claim 6; SEQ ID NO 3; 90pp; English.
XX
XX The invention relates to a method of converting a protein kinase C (PKC)
XX agonist peptide or peptidomimetic to a PKC antagonist peptide or
XX peptidomimetic, involving substituting at least one amino acid in the
XX agonist peptide or peptidomimetic with an amino acid that converts the
XX PKC agonist peptide or peptidomimetic into a PKC antagonist peptide or
XX peptidomimetic. The invention also relates to a method of inhibiting the
XX activity of a protein kinase C (PKC) enzyme, involving contacting the

CC enzyme with a PKC inhibitor peptide or peptidomimetic, the peptide
CC derived from a PKC agonist peptide or peptidomimetic where at least one
CC amino acid in the agonist peptide or peptidomimetic is substituted with
CC another amino acid sufficient to convert the peptide or peptidomimetic
CC into an antagonist peptide or peptidomimetic. The method is useful for
CC converting a PKC agonist peptide or peptidomimetic to a PKC antagonist
CC peptide or peptidomimetic. The antagonist peptide is useful for treating
CC a disease or condition modulated by epsilon-PKC such as scleroderma,
CC fibrosis or pulmonary fibrosis, septic shock, ischemia, inflammatory
CC bowel disease, autoimmune disease e.g. multiple sclerosis, Guillain Barre
CC syndrome, psoriasis, Graves disease, rheumatoid arthritis, diabetes
CC mellitus and pulmonary disease e.g. chronic obstructive pulmonary disease
CC and asthma. This sequence represents a receptor for activated C kinase
CC (RACK) peptide used in the method of the invention.
XX
SQ Sequence 8 AA;
Query Match 100.0%; Score 48; DB 9; Length 8;
Best Local Similarity 100.0%; Pred. No. 2e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 HDAPICGD 8
Db 1 HDAPICGD 8
RESULT 5
AEA89971
ID AEA89971 standard; peptide, 30 AA.
AC AEA89971;
XX 08-SEP-2005 (first entry)
XX Receptor for activated C kinase (RACK) peptide #9.
XX
XX Protein interaction; protein kinase C; epsilon-PKC; scleroderma;
KM fibrosis; pulmonary fibrosis; septic shock; ischemia;
KM inflammatory bowel disease; autoimmune disease; multiple sclerosis;
KM Guillain Barre syndrome; psoriasis; Graves disease; rheumatoid arthritis;
KM diabetes mellitus; pulmonary disease;
KM chronic obstructive pulmonary disease; asthma;
KM receptor for activated C kinase; RACK; anti-inflammatory; dermatological;
KM hepatotropic; respiratory-gen.; immunosuppressive; neuroprotective;
KM antiproliferative; CNS-gen.; antithyroid; antidiabetic; antirheumatic;
KM antidiabetic; antidiabetic; gastrointestinal-gen.; antibacterial;
KM vasotropic; cardiant.
OS Homo sapiens.
XX
XX WO2005059124-A2.
XX
XX 30-JUN-2005.
XX
XX 13-DEC-2004; 2004WO-US041854.
XX
XX 11-DEC-2003; 2003US-0529223P.
XX
XX (STRD) UNIV LELAND STANFORD JUNIOR.
XX
XX Mochly-Rosen D, Chen LE;
XX
XX WPI; 2005-479333/48.
XX
XX Converting protein kinase C (PKC) agonist peptide to PKC antagonist
XX peptide useful for treating fibrotic or inflammatory disease, involves
XX substituting charged amino acid in agonist peptide with another uncharged
XX amino acid.
XX
XX Disclosure; SEQ ID NO 93; 90pp; English.
XX
XX The invention relates to a method of converting a protein kinase C (PKC)
XX agonist peptide or peptidomimetic to a PKC antagonist peptide or

CC peptidomimetic, involving substituting at least one amino acid in the
 CC agonist peptide or peptidomimetic with an amino acid that converts the
 CC PKC agonist peptide or peptidomimetic into a PKC antagonist peptide or
 CC peptidomimetic. The invention also relates to a method of inhibiting the
 CC activity of a protein kinase C (PKC) enzyme, involving contacting the
 CC enzyme with a PKC inhibitor peptide or peptidomimetic, the peptide
 CC derived from a PKC agonist peptide or peptidomimetic, where at least one
 CC amino acid in the agonist peptide or peptidomimetic is substituted with
 CC another amino acid sufficient to convert the peptide or peptidomimetic
 CC into an antagonist peptide or peptidomimetic. The method is useful for
 CC converting a PKC agonist peptide or peptidomimetic to a PKC antagonist
 CC peptide or peptidomimetic. The antagonist peptide is useful for treating
 CC a disease or condition modulated by epsilon-PKC such as scleroderma,
 CC fibrosis or pulmonary fibrosis, septic shock, ischemia, inflammatory
 CC bowel disease, autoimmune disease e.g. multiple sclerosis, Guillain Barre
 CC syndrome, psoriasis, Graves disease, rheumatoid arthritis, diabetes
 CC mellitus and pulmonary disease e.g. chronic obstructive pulmonary disease
 CC and asthma. This sequence represents a receptor for activated C kinase
 CC (RACK) peptide used in the method of the invention.

XX Sequence 30 AA;

Query Match 100.0%; Score 48; DB 9; Length 30;
 Best Local Similarity 100.0%; Pred. No. 0.056; Mismatches 0; Gaps 0;
 Matches 8; Conservative 0; Indels 0;

Qy 1 HDAPIGYD 8
 |||||
 Db 15 HDAPIGYD 22

RESULT 6
 AA018490
 ID AA018490 standard; protein; 737 AA.

AC AA018490;

XX 11-OCT-2002 (first entry)

DE Human Insulin receptor signaling modifier SEQ ID NO: 2.

KM Human; insulin receptor signaling; insulin receptor signaling modifier;
 KM ISM; diabetes; metabolic syndrome; antidiabetic.

OS Homo sapiens.

PN MO200255664-AA2.

PD 18-JUL-2002.

PF 11-JAN-2002; 2002WO-US001048.

PR 12-JAN-2001; 2001US-0261226P.

PR 12-JAN-2001; 2001US-0261303P.

PR 12-JAN-2001; 2001US-0261304P.

PR 12-JAN-2001; 2001US-0261335P.

PR 12-JAN-2001; 2001US-0261361P.

PR 12-JAN-2001; 2001US-0261456P.

PR 12-JAN-2001; 2001US-0261457P.

PR 12-JAN-2001; 2001US-0261458P.

PR 12-JAN-2001; 2001US-0261518P.

PR 12-JAN-2001; 2001US-0261531P.

PR 12-JAN-2001; 2001US-0261532P.

PR 12-JAN-2001; 2001US-0261589P.

PR 12-JAN-2001; 2001US-0261590P.

EXBLIXIS INC.

XX Seidel-Dugan C, Ferguson KC, Kidd T;
 PI WPI; 2002-559664/64.
 DR N-PSDB; AAL48609.

PT Identifying an insulin receptor signaling modulator, useful as drug
 PT targets for treating diabetes or metabolic disorders, comprises
 PT contacting an assay system comprising insulin receptor signaling
 PT modifiers with a test agent.

PS Disclosure; Page 32-35; 232pp; English.

XX The present invention relates to a method of identifying a candidate
 CC Insulin receptor (INR) signaling modulating agent, involving contacting
 CC an assay system comprising an insulin receptor signaling modifier (ISM)
 CC polypeptide or nucleic acid with a test agent, and detecting a test agent
 CC biased activity of the assay system. The method is useful for
 CC identifying candidate INR signaling modulating agents. ISM genes may be
 CC used as drug targets for treatment of disorders related to INR signaling
 CC such as diabetes or metabolic syndrome. ISM nucleic acids and
 CC polypeptides are useful for identifying and testing agents that modulate
 CC ISM function and for other applications related to the involvement of ISM
 CC in INR signaling, and for identifying subjects having a predisposition to
 CC such diseases associated with INR signaling. The present sequence is an
 CC ISM protein described in the exemplification of the invention

XX Sequence 737 AA;

Query Match 100.0%; Score 48; DB 5; Length 737;
 Best Local Similarity 100.0%; Pred. No. 1.7; Mismatches 0; Gaps 0;
 Matches 8; Conservative 0; Indels 0;

Qy 1 HDAPIGYD 8
 |||||
 Db 85 HDAPIGYD 92

RESULT 7
 ADA50073
 ID ADA50073 standard; protein; 737 AA.

AC ADA50073;

DE 20-NOV-2003 (first entry)

DE Mouse protein kinase C protein related to mouse skin cancer models.

XX UV radiation; human skin; non-human animal skin; FVB/N mouse;

KM human cancer; epithelial tissue; non-melanoma skin cancer; NMSC;

KM squamous cell carcinoma; SSC; animal model system; transgenic animal;

KM cancer development; cancer progression; cancer treatment;

KM protein kinase C; PKC; mouse epidermis; cyclostatic; vulnary;

KM dermatological; cell therapy; photodamage; photocaging; skin wounding;

KM PKC transgene; mouse; T7 tag; enzyme; protein kinase C epsilon.

OS Chimeric.

OS Mus musculus.

OS Enterobacteria phage T7.

PN US2003051258-A1.

PD 13-MAR-2003.

PF 27-AUG-2002; 2002US-00228931.

PR 30-JAN-2001; 2001US-00772647.

PA (VERMA/) VERMA A K.

PA (WHEELER/) WHEELER D L.

XX Verma AK, Wheeler DL;

DR WPI; 2003-596530/56.
 DR N-PSDB; ADA50078.
 XX
 PT Identifying an agent for reducing or preventing an effect of UV radiation
 PT on animal skin for treating or preventing e.g., squamous cell carcinoma
 PT by exposing an FVB/N mouse and administering at least one agent.
 PS Disclosure; Page 14-16; 18pp; English.
 XX
 CC This invention relates to a novel method for the identification of an
 CC agent for reducing or preventing an effect of UV radiation on skin of a
 CC human or non-human animal. The preferred method of the invention
 CC comprises exposing an FVB/N mouse to UV radiation and administering at
 CC least one agent. A majority of human cancers originate from epithelial
 CC tissue, for example non-melanoma skin cancer (NMSC) and squamous cell
 CC carcinoma (SCC). As such, there is a need for a good animal model system
 CC for studying how these cancers develop, progress and can be treated. The
 CC present invention provides an FVB/N mouse that expresses more protein
 CC kinase C (PKC) in its epidermis than that of a wild-type mouse which may
 CC be a useful model for development and treatment of skin cancer,
 CC particularly SCC, in human and non-human mammalian animals. The invention
 CC may provide a method for the development of compounds with cytostatic,
 CC vulnary or dermatological activity through use in cell therapy. The
 CC method may therefore prove useful for preparing a composition for treating
 CC or preventing SCC, photocarcinoma, photocaging or skin wounding induced by UV
 CC radiation. The present sequence is that of mouse protein kinase C (PKC)
 CC with a 5' T7 tag, the coding DNA sequence of which was used in the
 CC production of a PKC transgene during the exemplification of the
 CC invention.
 CC
 CC Sequence 737 AA;
 SQ
 Query Match 100.0%; Score 48; DB 6; Length 737;
 Best Local Similarity 100.0%; Pred. No. 1.7;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 HDAPIGYD 8
 |||||
 DB 85 HDAPIGYD 92
 RESULT 8
 AAE39167
 ID AAE39167 standard; protein; 737 AA.
 XX
 AC AAE39167;
 XX
 DT 18-DEC-2003 (first entry)
 XX
 DE Mouse protein kinase C-epsilon -T7 tag chimeric protein.
 XX
 KW Mouse; protein kinase C-epsilon; PKC-epsilon; squamous cell carcinoma;
 KW SCC; skin cancer; enzyme; chimeric; fusion protein.
 XX
 OS Chimeric- Mus musculus.
 OS Chimeric- Bacteriophage T7.
 XX
 PN US6521815-B1.
 XX
 PD 18-FEB-2003.
 PD
 PF 30-JAN-2001; 2001US-00772647.
 PF
 PR 30-JAN-2001; 2001US-00772647.
 PR
 PA (WISC) WISCONSIN ALUMNI RES FOUND.
 PA
 PI Verma AK, Reddig PJ, Jansen AP;
 PI
 XX WPI; 2003-352430/33.
 DR N-PSDB; AAD59551.
 DR
 XX Novel genetically modified FVB/N mouse having epidermal cells that

PT comprise a protein kinase C-epsilon activity higher than that of wild-
 PT type FVB/N epidermal cells, for investigating development of metastatic
 PT disease.
 XX
 PS Disclosure; Col 23-28; 16pp; English.
 XX
 CC The present invention provides novel genetically modified FVB/N mouse
 CC having epidermal cells that comprise a protein kinase C (PKC)-epsilon
 CC activity higher than that of wild-type FVB/N epidermal cells. The
 CC invention is useful for evaluating the effectiveness of a putative agent
 CC as a chemopreventive agent against squamous cell carcinoma (SCC) disease in a
 CC mammal by administering one putative agent to papilloma-suppressed FVB/N
 CC mice having epidermal cells that comprise PKC-epsilon activity higher
 CC than that of wild type FVB/N epidermal cells. The invention is also
 CC useful as a tool for investigating the development of metastatic disease,
 CC for screening putative agents for altering susceptibility, development
 CC and progression of squamous cell carcinoma and metastatic squamous cell
 CC carcinoma and as a model for the development and treatment of metastatic
 CC skin cancer particularly squamous cell carcinoma in human and non-human
 CC mammalian animals. The present sequence is mouse protein kinase C-epsilon
 CC -T7 tag chimeric protein
 CC
 CC Sequence 737 AA;
 SQ
 Query Match 100.0%; Score 48; DB 7; Length 737;
 Best Local Similarity 100.0%; Pred. No. 1.7;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 HDAPIGYD 8
 |||||
 DB 85 HDAPIGYD 92
 RESULT 9
 ADE57469
 ID ADE57469 standard; protein; 737 AA.
 XX
 AC ADE57469;
 XX
 DT 29-JAN-2004 (first entry)
 XX
 DE Human Protein Q02156, SEQ ID NO 3331.
 XX
 KW Human; pain; neuronal tissue; gene therapy;
 KW spinal segmental nerve injury; chronic constriction injury; CCI;
 KW spared nerve injury; SWI; Chung.
 XX
 OS Homo sapiens.
 OS
 PN WO2003016475-A2.
 PN
 PD 27-FEB-2003.
 PD
 PF 14-AUG-2002; 2002WO-US025765.
 PF
 PR 14-AUG-2001; 2001US-0112147P.
 PR 01-NOV-2001; 2001US-0346382P.
 PR 26-NOV-2001; 2001US-0333347P.
 XX
 PA (GENO) GEN HOSPITAL CORP.
 PA
 PI (FARB) BAYER AG.
 PI
 XX Woolf C, D'Urso D, Befort K, Costigan M;
 XX
 DR WPI; 2003-268312/26.
 DR
 DR GENBANK; Q02156.
 DR
 PT New composition comprising two or more isolated polypeptides, useful for
 PT preparing a medicament for treating pain in an animal.
 PT
 PS Claim 1; Page; 1017pp; English.
 PS
 CC The invention discloses a composition comprising two or more isolated rat

CC or human polynucleotides or a polynucleotide which represents a fragment,
CC derivative or allelic variation of the nucleic acid sequence. Also
CC claimed are a vector comprising the novel polynucleotide, a host cell
CC comprising the vector, a method for identifying a nucleotide sequence
CC which is differentially regulated in an animal subjected to pain and a
CC kit to perform the method, an array, a method for identifying an agent
CC that increases or decreases the expression of the polynucleotide sequence
CC that is differentially expressed in neuronal tissue of a first animal
CC subjected to pain, a method for identifying a compound which regulates
CC the expression of a polynucleotide sequence which is differentially
CC expressed in an animal subjected to pain, a method for identifying a
CC compound that regulates the activity of one or more of the
CC polynucleotides, a method for producing a pharmaceutical composition, a
CC method for identifying a compound or small molecule that regulates the
CC activity in an animal of one or more of the polypeptides given in the
CC specification, a method for identifying a compound useful in treating
CC pain and a pharmaceutical composition comprising the one or more
CC polypeptides or their antibodies. The polynucleotide or the compound that
CC modulates its activity is useful for preparing a medicament for treating
CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
CC therapy). The sequence presented is a human protein (shown in Table 2 of
CC the specification) which is differentially expressed during pain. Note:
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic form directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.

SQ Sequence 737 AA;

Query Match 100.0%; Score 48; DB 7; Length 737;

Best Local Similarity 100.0%; Pred. No. 1.7;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 HDAPRGYD 8
Db 85 HDAPRGYD 92RESULT 10
ADES7541
ID ADES7541 standard; protein; 737 AA.

AC ADES7541;

DT 29-JAN-2004 (first entry)

DE Human Protein Q02156, SEQ ID NO 3403.

XX Human; pain; neuronal tissue; gene therapy;
KW spinal segmental nerve injury; chronic constriction injury; CCI;
XX spared nerve injury; SNI; Chung.

OS Homo sapiens.

PN WO2003016475-A2.

PD 27-FEB-2003.

PF 14-AUG-2002; 2002WO-US025765.

PR 14-AUG-2001; 2001US-0312147P.

PR 01-NOV-2001; 2001US-0346382P.

PR 26-NOV-2001; 2001US-0333347P.

PA (GENO) GEN HOSPITAL CORP.

PA (FARB) BAYER AG.

PI 2003-268312/26.

Position comprising two or more isolated polypeptides, useful for

PT preparing a medicament for treating pain in an animal.
XX Claim 1; Page; 1017pp; English.

XX The invention discloses a composition comprising two or more isolated rat
CC or human polynucleotides or a polynucleotide which represents a fragment,
CC derivative or allelic variation of the nucleic acid sequence. Also
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CC the expression of a polynucleotide sequence which is differentially
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CC method for identifying a compound or small molecule that regulates the
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CC specification, a method for identifying a compound useful in treating
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CC modulates its activity is useful for preparing a medicament for treating
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CC ftp.wipo.int/pub/published_pct_sequences.

SQ Sequence 737 AA;

Query Match 100.0%; Score 48; DB 7; Length 737;

Best Local Similarity 100.0%; Pred. No. 1.7;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 HDAPRGYD 8
Db 85 HDAPRGYD 92RESULT 11
ADES8354
ID ADES8354 standard; protein; 737 AA.

AC ADES8354;

DT 29-JAN-2004 (first entry)

DE Human Protein Q02156, SEQ ID NO 4228.

XX Human; pain; neuronal tissue; gene therapy;
KW spinal segmental nerve injury; chronic constriction injury; CCI;
XX spared nerve injury; SNI; Chung.

OS Homo sapiens.

PN WO2003016475-A2.

PD 27-FEB-2003.

PF 14-AUG-2002; 2002WO-US025765.

PR 14-AUG-2001; 2001US-0312147P.

PR 01-NOV-2001; 2001US-0346382P.

PR 26-NOV-2001; 2001US-0333347P.

PA (GENO) GEN HOSPITAL CORP.

PA (FARB) BAYER AG.

PI 2003-268312/26.

Position comprising two or more isolated polypeptides, useful for

XX WPI: 2003-268312/26.
 DR GENBANK: Q02156.
 XX
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 PT preparing a medicament for treating pain in an animal.
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 CC or human polynucleotides or a polynucleotide which represents a fragment,
 CC derivative or allelic variation of the nucleic acid sequence. Also
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 CC that is differentially expressed in neuronal tissue of a first animal
 CC subjected to pain, a method for identifying a compound which regulates
 CC the expression of a polynucleotide sequence which is differentially
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 CC ftp.wipo.int/pub/published_pct_sequences.
 XX
 SO Sequence 737 AA:
 Query Match 100.0%; Score 48; DB 7; Length 737;
 Best Local Similarity 100.0%; Pred. No. 1.7;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 HDAPRGYD 8
 DB 85 HDAPRGYD 92
 RESULT 12
 ADE57531
 ID ADE57531 standard; protein: 737 AA.
 XX
 AC ADE57531;
 XX
 DT 29-JAN-2004 (first entry)
 XX
 DE Rat Protein AAA1872, SEQ ID NO 3393.
 XX
 KW Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury;
 KW chronic constriction injury; CCI; spared nerve injury; SNI; Chung.
 XX
 OS Rattus norvegicus.
 XX
 PN WO2003016475-A2.
 PD 27-FEB-2003.
 XX
 PF 14-AUG-2002; 2002WO-US025765.
 XX
 PR 14-AUG-2001; 2001US-0312147P.
 PR 01-NOV-2001; 2001US-0346382P.
 PR 26-NOV-2001; 2001US-0333347P.
 XX

PA (GENO) GEN HOSPITAL CORP.
 PA (FARB) BAYER AG.
 XX
 PT Woolf C, D'urso D, Befort K, Costigan M;
 XX
 DR WPI: 2003-268312/26.
 DR GENBANK: AAA1872.
 XX
 PT New composition comprising two or more isolated polypeptides, useful for
 PT preparing a medicament for treating pain in an animal.
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 PS Claim 1, Page: 1017pp; English.
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 CC or human polynucleotides or a polynucleotide which represents a fragment,
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 CC ftp.wipo.int/pub/published_pct_sequences.
 XX
 SO Sequence 737 AA:
 Query Match 100.0%; Score 48; DB 7; Length 737;
 Best Local Similarity 100.0%; Pred. No. 1.7;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 HDAPRGYD 8
 DB 85 HDAPRGYD 92
 RESULT 13
 ADE57533
 ID ADE57533 standard; protein: 737 AA.
 XX
 AC ADE57533;
 XX
 DT 29-JAN-2004 (first entry)
 XX
 DE Human Protein Q02156, SEQ ID NO 3395.
 XX
 KW Human; pain; neuronal tissue; gene therapy;
 KW spinal segmental nerve injury; chronic constriction injury; CCI;
 KW spared nerve injury; SNI; Chung.
 XX
 OS Homo sapiens.
 XX
 PN WO2003016475-A2.
 PD 27-FEB-2003.
 XX
 PF 14-AUG-2002; 2002WO-US025765.
 XX

XX 14-AUG-2001; 2001US-0312147P.
PR 01-NOV-2001; 2001US-0346382P.
PR 26-NOV-2001; 2001US-0333347P.
XX
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
XX
PI Woolf C, D'urso D, Befort K, Costigan M;
XX WPI; 2003-268312/26.
DR GENBANK; Q02156.
XX
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PT preparing a medicament for treating pain in an animal.
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CC or human polynucleotides or a polynucleotide which represents a fragment,
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CC ftp.wipo.int/pub/published_pct_sequences.
CC
XX SQ Sequence 737 AA;
SQ
Query Match 100.0%; Score 48; DB 7; Length 737;
Best Local Similarity 100.0%; Pred. No. 1.7;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 HDAPIGYD 8
DB 85 HDAPIGYD 92
DB
RESULT 14
ADES8352
ID ADE58352 standard; protein; 737 AA.
XX
AC ADE58352;
XX
DT 29-JAN-2004 (first entry)
XX
DE Rat Protein KRTCE, SEQ ID NO 4226.
XX
KW Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury;
XX chronic constriction injury; CCI; spared nerve injury; SNI; Chung.
XX
XX 016475-A2.

XX 27-FEB-2003.
XX
PD 14-AUG-2002; 2002MO-US025765.
XX
PF 14-AUG-2001; 2001US-0312147P.
XX
PR 01-NOV-2001; 2001US-0346382P.
PR 26-NOV-2001; 2001US-0333347P.
XX
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
XX
PI Woolf C, D'urso D, Befort K, Costigan M;
XX WPI; 2003-268312/26.
DR
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PT preparing a medicament for treating pain in an animal.
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CC ftp.wipo.int/pub/published_pct_sequences.
CC
XX SQ Sequence 737 AA;
SQ
Query Match 100.0%; Score 48; DB 7; Length 737;
Best Local Similarity 100.0%; Pred. No. 1.7;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 HDAPIGYD 8
DB 85 HDAPIGYD 92
DB
RESULT 15
ADE57535
ID ADE57535 standard; protein; 737 AA.
XX
AC ADE57535;
XX
DT 29-JAN-2004 (first entry)
XX
DE Rat Protein AAA41872, SEQ ID NO 3397.
XX
KW Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury;
XX chronic constriction injury; CCI; spared nerve injury; SNI; Chung.
XX

OS Rattus norvegicus.
 XX WO2003016475-A2.
 XX 27-FEB-2003.
 XX 14-AUG-2002; 2002WO-US025765.
 XX 14-AUG-2001; 2001US-0312147P.
 PR 01-NOV-2001; 2001US-0346382P.
 PR 26-NOV-2001; 2001US-0333347P.
 XX (GHEO) GEN HOSPITAL CORP.
 PA (FARB) BAYER AG.
 XX Woolf C, D'urso D, Befort K, Costigan M;
 PI WPI; 2003-268312/26.
 DR GENBANK; AAA41872.
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 CC ftp.wipo.int/pub/published_pct_sequences.
 CC
 XX Sequence 737 AA;
 SQ
 QY Query Match 100.0%; Score 48; DB 7; Length 737;
 Db Best Local Similarity 100.0%; Pred. No. 1.7;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 1 HDAPIGYD 8
 85 HDAPIGYD 92
 RESULT 16
 ADE57537
 ID ADE57537 standard; protein; 737 AA.
 XX
 XX AC ADE57537;
 XX
 DT 29-JAN-2004 (first entry)
 XX
 XX Human Protein Q02156, SEQ ID NO 3399.
 DE

XX
 KW Human; pain; neuronal tissue; gene therapy;
 KW spinal segmental nerve injury; chronic constriction injury; CCI;
 KW spared nerve injury; SNI; Chung.
 XX
 OS Homo sapiens.
 XX WO2003016475-A2.
 XX 27-FEB-2003.
 XX 14-AUG-2002; 2002WO-US025765.
 XX 14-AUG-2001; 2001US-0312147P.
 PR 01-NOV-2001; 2001US-0346382P.
 PR 26-NOV-2001; 2001US-0333347P.
 XX (GHEO) GEN HOSPITAL CORP.
 PA (FARB) BAYER AG.
 XX Woolf C, D'urso D, Befort K, Costigan M;
 PI WPI; 2003-268312/26.
 DR GENBANK; Q02156.
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 CC ftp.wipo.int/pub/published_pct_sequences.
 CC
 XX Sequence 737 AA;
 SQ
 QY Query Match 100.0%; Score 48; DB 7; Length 737;
 Db Best Local Similarity 100.0%; Pred. No. 1.7;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 1 HDAPIGYD 8
 85 HDAPIGYD 92
 RESULT 17
 ADE57539
 ID ADE57539 standard; protein; 737 AA.
 XX

AC ADE57539;
XX
XX 29-JAN-2004 (first entry)
XX
XX
DE Rat Protein AAA41872, SEQ ID NO 3401.
XX
XX Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury;
XX chronic constriction injury; CCI; spared nerve injury; SNI; Chung.
XX
XX Rattus norvegicus.
XX
XX MO2003016475-A2.
XX
XX 27-FEB-2003.
XX
XX 14-AUG-2002; 2002WO-US025765.
XX
XX 14-AUG-2001; 2001US-0312147P.
XX 01-NOV-2001; 2001US-0346382P.
XX 26-NOV-2001; 2001US-0333347P.
XX
XX (GENO) GEN HOSPITAL CORP.
XX (FARB) BAYER AG.
XX
XX Woolf C, D'Urso D, Befort K, Costigan M;
XX
XX WPI; 2003-268312/26.
XX GENBANK; AAA41872.
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XX
XX Sequence 737 AA;
XX
XX Query Match 100.0%; Score 48; DB 7; Length 737;
XX Best Local Similarity 100.0%; Pred. NO. 1.7;
XX Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 18
ADE57527
XX ID ADE57527 standard; protein; 737 AA.
XX
XX AC ADE57527;
XX
XX 29-JAN-2004 (first entry)
XX
XX Rat Protein AAA41872, SEQ ID NO 3389.
XX
XX Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury;
XX chronic constriction injury; CCI; spared nerve injury; SNI; Chung.
XX
XX Rattus norvegicus.
XX
XX OS
XX MO2003016475-A2.
XX
XX 27-FEB-2003.
XX
XX 14-AUG-2002; 2002WO-US025765.
XX
XX 14-AUG-2001; 2001US-0312147P.
XX 01-NOV-2001; 2001US-0346382P.
XX 26-NOV-2001; 2001US-0333347P.
XX
XX (GENO) GEN HOSPITAL CORP.
XX (FARB) BAYER AG.
XX
XX Woolf C, D'Urso D, Befort K, Costigan M;
XX
XX WPI; 2003-268312/26.
XX GENBANK; AAA41872.
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XX compound that regulates the activity of one or more of the
XX polynucleotides, a method for producing a pharmaceutical composition, a
XX method for identifying a compound or small molecule that regulates the
XX activity in an animal of one or more of the polypeptides given in the
XX specification, a method for identifying a compound useful in treating
XX pain and a pharmaceutical composition comprising the one or more
XX polypeptides or their antibodies. The polynucleotide or the compound that
XX modulates its activity is useful for preparing a medicament for treating
XX pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
XX injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
XX therapy). The sequence presented is a rat protein (shown in Table 2 of
XX the specification) which is differentially expressed during pain. Note:
XX The sequence data for this patent did not form part of the printed
XX specification, but was obtained in electronic form directly from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences.
XX
XX Sequence 737 AA;
XX
XX Query Match 100.0%; Score 48; DB 7; Length 737;
XX Best Local Similarity 100.0%; Pred. No. 1.7;
XX Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 HDAPIGYD 8
|||||||
85 HDAPIGYD 92

1 HDAPIGYD 8
|||||||
85 HDAPIGYD 92

Db 85 HDAPIGYD 92

RESULT 19

AD57529
ID AD57529 standard; protein; 737 AA.

AC AD57529;

DT 29-JAN-2004 (first entry)

DE Human Protein Q02156, SEQ ID NO 3391.

DE Human; pain; neuronal tissue; gene therapy;

KW spinal segmental nerve injury; chronic constriction injury; CCI;

KW spared nerve injury; SNI; Chung.

OS Homo sapiens.

PN W02003016475-A2.

PD 27-FEB-2003.

PF 14-AUG-2002; 2002WO-US025765.

PR 14-AUG-2001; 2001US-0312147P.

PR 01-NOV-2001; 2001US-0346382P.

PR 26-NOV-2001; 2001US-0333347P.

PA (GENO) GEN HOSPITAL CORP.

PI (FARB) BAYER AG.

PI Woolf C, D'Urso D, Befort K, Costigan M;

DR WPI; 2003-268312/26.

DR GENBANK; 002156.

PT New composition comprising two or more isolated polypeptides, useful for

PT preparing a medicament for treating pain in an animal.

PS Claim 1; Page: 1017pp; English.

XX The invention discloses a composition comprising two or more isolated rat

CC or human polynucleotides or a polynucleotide which represents a fragment,

CC derivative or allelic variation of the nucleic acid sequence. Also

CC claimed are a vector comprising the novel polynucleotide, a host cell

CC comprising the vector, a method for identifying a nucleotide sequence

CC which is differentially regulated in an animal subjected to pain and a

CC kit to perform the method, an array, a method for identifying an agent

CC that increases or decreases the expression of the polynucleotide sequence

CC that is differentially expressed in neuronal tissue of a first animal

CC subjected to pain, a method for identifying a compound which regulates

CC the expression of a polynucleotide sequence which is differentially

CC expressed in an animal subjected to pain, a method for identifying a

CC compound that regulates the activity of one or more of the

CC polynucleotides, a method for producing a pharmaceutical composition, a

Query Match 100.0%; Score 48; DB 7; Length 737;
Best Local Similarity 100.0%; Pred. No. 1.7;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HDAPIGYD 8
Db 85 HDAPIGYD 92

RESULT 20

ADY80150
ID ADY80150 standard; protein; 737 AA.

AC ADY80150;

DT 02-JUN-2005 (first entry)

DE Amino acid sequence of human protein kinase C epsilon K437R mutant.

DE protein kinase C epsilon; PKCε; glucose metabolism; insulin;

KW antidiabetic; protein kinase C epsilon antagonist;

KW non-insulin dependent diabetes; endocrine disease; hyperglycemia;

KW hyperinsulinemia; insulin resistance; glucose intolerance.

OS Homo sapiens.

PN W02005025602-A1.

PD 24-MAR-2005.

PF 16-SEP-2004; 2004WO-AU001255.

PR 16-SEP-2003; 2003AU-00905421.

PR 22-JUL-2004; 2004AU-00904077.

PA (GARV-) GARVAN INST MEDICAL RES.

PI Biden TJ, Schmitz-Pelffer C;

DR WPI; 2005-253847/26.

PT Determining an antagonist of a protein kinase C epsilon (PKCε) for

PT treating abnormal glucose metabolism in subject comprises determining the

PT rate of internalization of the insulin receptor in the insulin-stimulated

PT hepatocytes.

PS Disclosure; SEQ ID NO 14; 138pp; English.

XX The specification describes a method for identifying modulators of

CC protein kinase C epsilon (PKCε) for the treatment of abnormal glucose

CC metabolism in a human or animal subject. The method comprises incubating

CC a hepatocyte in the presence and absence of a candidate compound;

CC stimulating the hepatocytes with insulin or its analogue; and determining

CC the rate of internalization of the insulin receptor in the insulin-

CC stimulated hepatocytes, where reduced insulin receptor internalization in

CC the presence of the candidate compound compared to in the absence of the

CC candidate compound indicates that the compound is an antagonist of PKCε.

CC The method is useful for treating abnormal glucose metabolism, e.g. Type

CC 2 diabetes, hyperglycemia, hyperinsulinemia, insulin resistance, or

CC glucose intolerance. The present sequence encodes the human PKCε K437R

Query Match 100.0%; Score 48; DB 9; Length 737;
Best Local Similarity 100.0%; Pred. No. 1.7;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HDAPIGYD 8
Db 85 HDAPIGYD 92

RESULT 21

ADY80138
XX ADY80138 standard; protein; 737 AA.

AC ADY80138;

DT 02-JUN-2005 (first entry)

XX Amino acid sequence of murine protein kinase C epsilon.

DE protein kinase C epsilon; PKCε; glucose metabolism; insulin;

KW antidiabetic; protein kinase C epsilon antagonist;

KW non-insulin dependent diabetes; endocrine disease; hyperglycemia;

XX hyperinsulinemia; insulin resistance; glucose intolerance.

OS Mus sp.

XX MO2005025602-A1.

XX 24-MAR-2005.

XX 16-SEP-2004; 2004WO-AU001255.

XX 16-SEP-2003; 2003AU-00905421.

XX 22-JUL-2004; 2004AU-00904077.

XX (GARV-) GARVAN INST MEDICAL RES.

XX Biden TJ, Schmitz-Peiffer C;

XX WPI; 2005-253847/26.

XX N-PSDB; ADY80137.

XX Determining an antagonist of a protein kinase C epsilon (PKCε) for

XX creating abnormal glucose metabolism in subject comprises determining the

XX rate of internalization of the insulin receptor in the insulin-stimulated

XX hepatocytes.

XX Claim 8; SEQ ID NO 2; 138pp; English.

XX The specification describes a method for identifying modulators of

XX protein kinase C epsilon (PKCε) for the treatment of abnormal glucose

XX metabolism in a human or animal subject. The method comprises incubating

XX a hepatocyte in the presence and absence of a candidate compound;

XX stimulating the hepatocytes with insulin or its analogue; and determining

XX the rate of internalization of the insulin receptor in the insulin-

XX stimulated hepatocytes, where reduced insulin receptor internalization in

XX the presence of the candidate compound compared to in the absence of the

XX candidate compound indicates that the compound is an antagonist of PKCε.

XX The method is useful for treating abnormal glucose metabolism, e.g. Type

XX 2 diabetes, hyperglycemia, hyperinsulinemia, insulin resistance, or

XX glucose intolerance. The present sequence represents a murine PKCε.

XX Sequence 737 AA;

Query Match 100.0%; Score 48; DB 9; Length 737;

Best Local Similarity 100.0%; Pred. No. 1.7; Mismatches 0; Indels 0; Gaps 0;

QY 1 HDAPIGYD 8

DB 85 HDAPIGYD 92

RESULT 22

ADY80140
XX ADY80140 standard; protein; 737 AA.

AC ADY80140;

DT 02-JUN-2005 (first entry)

XX Amino acid sequence of human protein kinase C epsilon.

DE protein kinase C epsilon; PKCε; glucose metabolism; insulin;

KW antidiabetic; protein kinase C epsilon antagonist;

KW non-insulin dependent diabetes; endocrine disease; hyperglycemia;

XX hyperinsulinemia; insulin resistance; glucose intolerance.

OS Homo sapiens.

XX MO2005025602-A1.

XX 24-MAR-2005.

XX 16-SEP-2004; 2004WO-AU001255.

XX 16-SEP-2003; 2003AU-00905421.

XX 22-JUL-2004; 2004AU-00904077.

XX (GARV-) GARVAN INST MEDICAL RES.

XX Biden TJ, Schmitz-Peiffer C;

XX WPI; 2005-253847/26.

XX N-PSDB; ADY80139.

XX Determining an antagonist of a protein kinase C epsilon (PKCε) for

XX creating abnormal glucose metabolism in subject comprises determining the

XX rate of internalization of the insulin receptor in the insulin-stimulated

XX hepatocytes.

XX Example 8; SEQ ID NO 4; 138pp; English.

XX The specification describes a method for identifying modulators of

XX protein kinase C epsilon (PKCε) for the treatment of abnormal glucose

XX metabolism in a human or animal subject. The method comprises incubating

XX a hepatocyte in the presence and absence of a candidate compound;

XX stimulating the hepatocytes with insulin or its analogue; and determining

XX the rate of internalization of the insulin receptor in the insulin-

XX stimulated hepatocytes, where reduced insulin receptor internalization in

XX the presence of the candidate compound compared to in the absence of the

XX candidate compound indicates that the compound is an antagonist of PKCε.

XX The method is useful for treating abnormal glucose metabolism, e.g. Type

XX 2 diabetes, hyperglycemia, hyperinsulinemia, insulin resistance, or

XX glucose intolerance. The present sequence represents a human PKCε.

XX Sequence 737 AA;

Query Match 100.0%; Score 48; DB 9; Length 737;

Best Local Similarity 100.0%; Pred. No. 1.7; Mismatches 0; Indels 0; Gaps 0;

QY 1 HDAPIGYD 8

DB 85 HDAPIGYD 92

RESULT 23

ADY80151
XX ADY80151 standard; protein; 737 AA.

AC ADY80151;

DT 02-JUN-2005 (first entry)

XX Amino acid sequence of murine protein kinase C epsilon K437R mutant.

DE protein kinase C epsilon; PKCε; glucose metabolism; insulin;

KW antidiabetic; protein kinase C epsilon antagonist;

KW non-insulin dependent diabetes; endocrine disease; hyperglycemia;

XX hyperinsulinemia; insulin resistance; glucose intolerance.

OS Mus sp.

XX XX WO2005025602-A1.
 XX XX
 XX XX 24-MAR-2005.
 XX XX
 XX XX 16-SEP-2004; 2004WO-AU001255.
 XX XX
 XX XX 16-SEP-2003; 2003AU-00905421.
 XX XX
 XX XX 22-JUL-2004; 2004AU-00904077.
 XX XX
 XX XX (GARV-) GARVAN INST MEDICAL RES.
 XX XX
 XX XX Biden TJ, Schmitz-Peiffer C;
 XX XX
 XX XX WPI; 2005-253847/26.
 XX XX
 XX XX Determining an antagonist of a protein kinase C epsilon (PKCε) for
 XX XX treating abnormal glucose metabolism in subject comprises determining the
 XX XX rate of internalization of the insulin receptor in the insulin-stimulated
 XX XX hepatocytes.
 XX XX
 XX XX Claim 75; SEQ ID NO 15; 138bp; English.
 XX XX
 XX XX The specification describes a method for identifying modulators of
 XX XX protein kinase C epsilon (PKCε) for the treatment of abnormal glucose
 XX XX metabolism in a human or animal subject. The method comprises incubating
 XX XX a hepatocyte in the presence and absence of its candidate compound;
 XX XX stimulating the hepatocytes with insulin or its analogue; and determining
 XX XX the rate of internalization of the insulin receptor in the insulin-
 XX XX stimulated hepatocytes, where reduced insulin receptor internalization in
 XX XX the presence of the candidate compound compared to in the absence of the
 XX XX candidate compound indicates that the compound is an antagonist of PKCε.
 XX XX The method is useful for treating abnormal glucose metabolism, e.g. Type
 XX XX 2 diabetes, hyperglycemia, hyperinsulinemia, insulin resistance, or
 XX XX glucose intolerance. The present sequence encodes the murine PKCε K437R
 XX XX mutant. This is a "kinase-dead" PKCε, which competes with wild type PKCε,
 XX XX thereby competitively inhibiting the activity of endogenous PKCε in a
 XX XX cell.
 XX XX
 XX XX Sequence 737 AA;
 XX XX
 XX XX Query Match 100.0%; Score 48; DB 9; Length 737;
 XX XX Best Local Similarity 100.0%; Pred. No. 1.7;
 XX XX Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0
 XX XX
 XX XX QY 1 HDAPIGYD 8
 XX XX |||||
 XX XX Db 85 HDAPIGYD 92
 XX XX
 XX XX RESULT 24
 XX XX ABB99506
 XX XX ID ABB99506 standard; peptide; 8 AA.
 XX XX
 XX XX AC ABB99506;
 XX XX
 XX XX DT 03-WAR-2003 (first entry)
 XX XX
 XX XX DE Amino acid sequence of a modified pseudo-epsilon RACK peptide.
 XX XX
 XX XX KW pseudo-epsilon RACK; RACK; receptor for activated C-kinase;
 XX XX protein kinase C; PKC; tissue damage; ischaemia; hypoxia.
 XX XX
 XX XX OS Synthetic.
 XX XX
 XX XX PN WO200278600-A2.
 XX XX
 XX XX PD 10-OCT-2002.
 XX XX
 XX XX PF 09-NOV-2001; 2001WO-US051600.
 XX XX
 XX XX PR 10-NOV-2000; 2000US-0247830P.
 XX XX

PA	(STRD) UNIV LELAND STANFORD JUNIOR.
XX	
PI	Mochly-Rosen D;
XX	
DR	WPI; 2003-092866/08.
XX	
PT	New composition comprising pseudo-epsilonRACK peptides, useful for
XX	
PS	treating tissue damage due to ischemia or hypoxia.
XX	
PS	Claim 6; Page 13; 30pp; English.
XX	
CC	The present sequence represents a modified pseudo-epsilon RACK
CC	occapeptide (see also ABB99501) . RACKs (receptors for activated C-kinase)
CC	are anchoring molecules, which selectively anchor activated protein
CC	kinase C (PKC) isozymes to their respective subcellular sites.
CC	Compositions comprising pseudo-epsilon RACK peptides are useful for
CC	reducing injury to a cell or tissue exposed to an ischaemic or hypoxic
CC	condition. The composition is useful for treating tissue damage due to
XX	ischaemia or hypoxia
XX	
SQ	Sequence 8 AA;
Query Match	91.7%; Score 44; DB 6; Length 8;
Best Local Similarity	87.5%; Pred. No. 2e+06;
Matches	7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
OY	1 HDAPIGYD 8
	:
Db	1 HDAPIGYE 8
RESULT 25	
ABB99512	
ID	ABB99512 standard; peptide; 8 AA.
XX	
AC	ABB99512;
XX	
DT	03-MAR-2003 (first entry)
XX	
DE	Amino acid sequence of a modified pseudo-epsilon RACK peptide.
XX	
KW	Pseudo-epsilon RACK; RACK; receptor for activated C-kinase;
XX	protein kinase C; PKC; tissue damage; ischemia; hypoxia.
OS	Synthetic.
XX	
PN	WO200278600-A2.
XX	
PD	10-OCT-2002.
XX	
PF	09-NOV-2001; 2001WO-US051600.
XX	
PR	10-NOV-2000; 2000US-0247830P.
XX	
PA	(STRD) UNIV LELAND STANFORD JUNIOR.
XX	
PI	Mochly-Rosen D;
XX	
DR	WPI; 2003-092866/08.
XX	
PT	New composition comprising pseudo-epsilonRACK peptides, useful for
XX	
PS	treating tissue damage due to ischemia or hypoxia.
XX	
PS	Claim 6; Page 13; 30pp; English.
XX	
CC	The present sequence represents a modified pseudo-epsilon RACK
CC	occapeptide (see also ABB99501) . RACKs (receptors for activated C-kinase)
CC	are anchoring molecules, which selectively anchor activated protein
CC	kinase C (PKC) isozymes to their respective subcellular sites.
CC	Compositions comprising pseudo-epsilon RACK peptides are useful for
CC	reducing injury to a cell or tissue exposed to an ischaemic or hypoxic
CC	condition. The composition is useful for treating tissue damage due to
CC	ischaemia or hypoxia

XX Sequence 8 AA;
SQ
Query Match 91.7%; Score 44; DB 6; Length 8;
Best Local Similarity 87.5%; Pred. No. 2e+06;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 HDAPIGYD 8
Db 1 HDGPIGYD 8

RESULT 26

ABG76125
ID ABG76125 standard; peptide; 8 AA.

XX AC ABG76125;

XX DT 07-MAY-2003 (first entry)

XX DE Pelepsilon RACK peptide #2.

XX KW Epsilon protein kinase C; epsilonPKC; RACK; ischaemia; hypoxia;

XX KM receptor for activated C-kinase; myocardial infarction;

XX KM cardiac ischaemia; peilepsilon RACK.

XX OS Synthetic.

XX PN US2002168354-A1.

XX PD 14-NOV-2002.

XX PF 09-NOV-2001; 2001US-00007363.

XX PR 10-NOV-2000; 2000US-0247830P.

XX PA (MOCH/) MOCHLY-ROSEN D.

XX PI Mochly-Rosen D;

XX DR WPI; 2003-092868/08.

XX PT New composition comprising pseudo-epsilonRACK peptides, useful for

XX PS creating tissue damage due to ischemia or hypoxia.

XX PS Claim 8; Page 6; 17pp; English.

XX CC The invention relates to reducing injury to a cell or tissue exposed to

XX CC an ischaemic or hypoxic condition, comprising administering to the cell

XX CC or tissue a peilepsilon Receptor for Activated C-Kinase (RACK) peptide.

XX CC The RACK peptide is an agonist of epsilon protein kinase C (epsilonPKC).

XX CC The method is useful in treating or protecting cells and tissues from

XX CC damage due to an ischaemic or hypoxic event, such as in cardiac ischaemia

XX CC or myocardial infarction. The present sequence is a peilepsilon RACK

XX CC peptide of the invention

XX SQ

Query Match 91.7%; Score 44; DB 6; Length 8;
Best Local Similarity 87.5%; Pred. No. 2e+06;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HDAPIGYD 8
Db 1 HDAPIGYD 8

RESULT 27

ABG76131

ABG76131 standard; peptide; 8 AA.

DT 07-MAY-2003 (first entry)

XX DE Pelepsilon RACK peptide #8.

XX KW Epsilon protein kinase C; epsilonPKC; RACK; ischaemia; hypoxia;

XX KM receptor for activated C-kinase; myocardial infarction;

XX KM cardiac ischaemia; peilepsilon RACK.

XX OS Synthetic.

XX PN US2002168354-A1.

XX PD 14-NOV-2002.

XX PF 09-NOV-2001; 2001US-00007363.

XX PR 10-NOV-2000; 2000US-0247830P.

XX PA (MOCH/) MOCHLY-ROSEN D.

XX PI Mochly-Rosen D;

XX DR WPI; 2003-092868/08.

XX PT New composition comprising pseudo-epsilonRACK peptides, useful for

XX PS creating tissue damage due to ischemia or hypoxia.

XX PS Claim 8; Page 6; 17pp; English.

XX CC The invention relates to reducing injury to a cell or tissue exposed to

XX CC an ischaemic or hypoxic condition, comprising administering to the cell

XX CC or tissue a peilepsilon Receptor for Activated C-Kinase (RACK) peptide.

XX CC The RACK peptide is an agonist of epsilon protein kinase C (epsilonPKC).

XX CC The method is useful in treating or protecting cells and tissues from

XX CC damage due to an ischaemic or hypoxic event, such as in cardiac ischaemia

XX CC or myocardial infarction. The present sequence is a peilepsilon RACK

XX CC peptide of the invention

XX SQ

Query Match 91.7%; Score 44; DB 6; Length 8;
Best Local Similarity 87.5%; Pred. No. 2e+06;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 HDAPIGYD 8
Db 1 HDGPIGYD 8

RESULT 28

AEA89893

AEA89893 standard; peptide; 8 AA.

XX ID AEA89893;

XX AC AEA89893;

XX DT 08-SEP-2005 (first entry)

XX DE Receptor for activated C kinase (RACK) peptide #15.

XX KW Protein interaction; protein kinase C; epsilon-PKC; scleroderma;

XX KM fibrosis; pulmonary fibrosis; septic shock; ischemia;

XX KM inflammatory bowel disease; autoimmune disease; multiple sclerosis;

XX KM Guillain Barre syndrome; psoriasis; Graves disease; rheumatoid arthritis;

XX KM diabetes mellitus; pulmonary disease;

XX KM chronic obstructive pulmonary disease; asthma;

XX KM receptor for activated C kinase; RACK; antiinflammatory; dermatological;

XX KM hepatotropic; respiratory-gen.; immunosuppressive; neuroprotective;

XX KM antiproliferative; CNS-gen.; antichyroid; antirheumatic;

XX KM antidiabetic; antiaesthetic; gastrointestinal-gen.; antibacterial;

XX KM vasotropic; cardiant.

XX OS Homo sapiens.

PN WO2005059124-A2.
 XX 30-JUN-2005.
 PD 13-DEC-2004; 2004WO-US041854.
 XX 11-DEC-2003; 2003US-0529223P.
 PR (STRD) UNIV LELAND STANFORD JUNIOR.
 PA Mochly-Rosen D, Chen LE;
 XX WPI; 2005-479333/48.
 DR
 XX
 XX Converting protein kinase C (PKC) agonist peptide to PKC antagonist
 PT peptide useful for treating fibrotic or inflammatory disease, involves
 PT substituting charged amino acid in agonist peptide with another uncharged
 PT amino acid.
 XX
 PS Disclosure; SEQ ID NO 15; 90pp; English.
 XX
 CC The invention relates to a method of converting a protein kinase C (PKC)
 CC agonist peptide or peptidomimetic to a PKC antagonist peptide or
 CC peptidomimetic, involving substituting at least one amino acid in the
 CC agonist peptide or peptidomimetic with an amino acid that converts the
 CC PKC agonist peptide or peptidomimetic into a PKC antagonist peptide or
 CC peptidomimetic. The invention also relates to a method of inhibiting the
 CC activity of a protein kinase C (PKC) enzyme, involving contacting the
 CC enzyme with a PKC inhibitor peptide or peptidomimetic, where the peptide
 CC derived from a PKC agonist peptide or peptidomimetic is substituted with
 CC amino acid in the agonist peptide or peptidomimetic is substituted with
 CC another amino acid sufficient to convert the peptide or peptidomimetic
 CC into an antagonist peptide or peptidomimetic. The method is useful for
 CC converting a PKC agonist peptide or peptidomimetic to a PKC antagonist
 CC peptide or peptidomimetic. The antagonist peptide is useful for treating
 CC a disease or condition modulated by epsilon-PKC such as scleroderma,
 CC fibrosis or pulmonary fibrosis, septic shock, ischemia, inflammatory
 CC bowel disease, autoimmune disease e.g. multiple sclerosis, Guillain Barre
 CC syndrome, psoriasis, Graves disease, rheumatoid arthritis, diabetes
 CC mellitus and pulmonary disease e.g. chronic obstructive pulmonary disease
 CC and asthma. This sequence represents a receptor for activated C kinase
 CC (RACK) peptide used in the method of the invention.
 CC
 XX
 SQ Sequence 8 AA;
 Query Match 91.7%; Score 44; DB 9; Length 8;
 Best Local Similarity 87.5%; Pred. No. 2e+06;
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Oy 1 HDAPIGVD 8
 Db 1 HDGPIGVD 8
 RESULT 29
 ID AEA89887 standard; peptide; 8 AA.
 XX AEA89887;
 AC
 XX 08-SEP-2005 (first entry)
 DT Receptor for activated C kinase (RACK) peptide #9.
 XX
 XX Protein interaction; protein kinase C; epsilon-PKC; scleroderma;
 KW fibrosis; pulmonary fibrosis; septic shock; ischemia;
 KW inflammatory bowel disease; autoimmune disease; multiple sclerosis;
 KW Guillain Barre syndrome; psoriasis; Graves disease; rheumatoid arthritis;
 KW diabetes mellitus; pulmonary disease;
 KW chronic obstructive pulmonary disease; asthma;
 KW receptor for activated C kinase; RACK; anti-inflammatory; dermatological;
 KW hepatotropic; respiratory-gen.; immunosuppressive; neuroprotective;
 KW antipeptidic; CNS-gen.; antihypertoid; antiarthritic; antirheumatic;

KW antidiabetic; antiasthmatic; gastrointestinal-gen.; antibacterial;
 KW vasotropic; cardiant.
 XX
 OS Homo sapiens.
 XX WO2005059124-A2.
 PN 30-JUN-2005.
 PD 13-DEC-2004; 2004WO-US041854.
 XX 11-DEC-2003; 2003US-0529223P.
 PR (STRD) UNIV LELAND STANFORD JUNIOR.
 PA Mochly-Rosen D, Chen LE;
 XX WPI; 2005-479333/48.
 DR
 XX
 XX Converting protein kinase C (PKC) agonist peptide to PKC antagonist
 PT peptide useful for treating fibrotic or inflammatory disease, involves
 PT substituting charged amino acid in agonist peptide with another uncharged
 PT amino acid.
 XX
 PS Disclosure; SEQ ID NO 9; 90pp; English.
 XX
 CC The invention relates to a method of converting a protein kinase C (PKC)
 CC agonist peptide or peptidomimetic to a PKC antagonist peptide or
 CC peptidomimetic, involving substituting at least one amino acid in the
 CC agonist peptide or peptidomimetic with an amino acid that converts the
 CC PKC agonist peptide or peptidomimetic into a PKC antagonist peptide or
 CC peptidomimetic. The invention also relates to a method of inhibiting the
 CC activity of a protein kinase C (PKC) enzyme, involving contacting the
 CC enzyme with a PKC inhibitor peptide or peptidomimetic, where the peptide
 CC derived from a PKC agonist peptide or peptidomimetic is substituted with
 CC amino acid in the agonist peptide or peptidomimetic is substituted with
 CC another amino acid sufficient to convert the peptide or peptidomimetic
 CC into an antagonist peptide or peptidomimetic. The method is useful for
 CC converting a PKC agonist peptide or peptidomimetic to a PKC antagonist
 CC peptide or peptidomimetic. The antagonist peptide is useful for treating
 CC a disease or condition modulated by epsilon-PKC such as scleroderma,
 CC fibrosis or pulmonary fibrosis, septic shock, ischemia, inflammatory
 CC bowel disease, autoimmune disease e.g. multiple sclerosis, Guillain Barre
 CC syndrome, psoriasis, Graves disease, rheumatoid arthritis, diabetes
 CC mellitus and pulmonary disease e.g. chronic obstructive pulmonary disease
 CC and asthma. This sequence represents a receptor for activated C kinase
 CC (RACK) peptide used in the method of the invention.
 CC
 XX
 SQ Sequence 8 AA;
 Query Match 91.7%; Score 44; DB 9; Length 8;
 Best Local Similarity 87.5%; Pred. No. 2e+06;
 Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 Oy 1 HDAPIGVD 8
 Db 1 HDAPIGVE 8
 RESULT 30
 ID AEA89909 standard; peptide; 8 AA.
 XX AEA89909;
 AC
 XX 08-SEP-2005 (first entry)
 DT Receptor for activated C kinase (RACK) peptide #1.
 XX
 XX Protein interaction; protein kinase C; epsilon-PKC; scleroderma;
 KW fibrosis; pulmonary fibrosis; septic shock; ischemia;
 KW inflammatory bowel disease; autoimmune disease; multiple sclerosis;
 KW Guillain Barre syndrome; psoriasis; Graves disease; rheumatoid arthritis;

KW diabetes mellitus; pulmonary disease;
 KW chronic obstructive pulmonary disease; asthma;
 KW receptor for activated C kinase; RACK; antiinflammatory; dermatological;
 KW hepatotropic; respiratory-gen.; immunosuppressive; neuroprotective;
 KW antipneumatic; CNS-gen.; antichryoid; antiarthritic; antirheumatic;
 KW antidiabetic; antiasclerotic; gastrointestinal-gen.; antibacterial;
 KW vasotropic; cardiac.

XX Homo sapiens.

XX WO2005059124-A2.

XX 30-JUN-2005.

XX 13-DEC-2004; 2004WO-US041854.

XX 11-DEC-2003; 2003US-0529223P.

XX (STRD) UNIV LELAND STANFORD JUNIOR.

XX Mochly-Rosen D, Chen LE;

XX WPI; 2005-479333/48.

XX The invention relates to a method of converting a protein kinase C (PKC)
 CC agonist peptide or peptidomimetic to a PKC antagonist peptide or
 CC peptidomimetic, involving substituting at least one amino acid in the
 CC agonist peptide or peptidomimetic with an amino acid that converts the
 CC PKC agonist peptide or peptidomimetic into a PKC antagonist peptide or
 CC peptidomimetic. The invention also relates to a method of inhibiting the
 CC activity of a protein kinase C (PKC) enzyme, involving contacting the
 CC enzyme with a PKC inhibitor peptide or peptidomimetic, the peptide
 CC derived from a PKC agonist peptide or peptidomimetic where at least one
 CC amino acid in the agonist peptide or peptidomimetic is substituted with
 CC another amino acid sufficient to convert the peptide or peptidomimetic
 CC into an antagonist peptide or peptidomimetic. The method is useful for
 CC converting a PKC agonist peptide or peptidomimetic to a PKC antagonist
 CC peptide or peptidomimetic. The antagonist peptide is useful for treating
 CC a disease or condition modulated by epsilon-PKC such as scleroderma,
 CC fibrosis or pulmonary fibrosis, septic shock, ischemia, inflammatory
 CC bowel disease, autoimmune disease e.g. multiple sclerosis, Guillain Barre
 CC syndrome, psoriasis, Graves disease, rheumatoid arthritis, diabetes
 CC mellitus and pulmonary disease e.g. chronic obstructive pulmonary disease
 CC and asthma. This sequence represents a receptor for activated C kinase
 CC (RACK) peptide used in the method of the invention.

XX Sequence 8 AA;

XX Query Match 91.7%; Score 44; DB 9; Length 8;
 XX Best Local Similarity 87.5%; Pred. No. 2e+06;
 XX Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 HDAPIGYD 8
 XX |||||
 DB 1 HDTPIGYD 8

RESULT 31

AAW54889
 ID AAW54889 standard; peptide; 8 AA.

XX AAW54889;

XX 4-SEP-1998 (first entry)

XX e-specific agonist peptide epsilon VI-7.5.

XX epsilon protein kinase C; ischaemic injury; hypoxic exposure.
 KW Synthetic.
 OS
 XX WO9817299-A1.

XX 30-APR-1998.

XX 17-OCT-1997; 97WO-US018716.

XX 18-OCT-1996; 96US-0028724P.

XX (STRD) UNIV LELAND STANFORD JUNIOR.

XX Mochly-Rosen D;

XX WPI; 1998-261181/23.

XX Peptide agonists of protein kinase C - used to reduce ischaemic injury of
 CC cells exposed to hypoxic conditions.

XX Disclosure; Page 32; 47pp; English.

XX The peptides AAW54879-W54901 are agonists of epsilon protein kinase C
 CC (PKC). They can be used for reducing ischaemic injury to a cell exposed
 CC to hypoxic conditions. They can also be used in a method for identifying
 CC a compound effective to induce preconditioning. The peptides are
 CC administered at a dose of 1-100 microgram administered once to several
 CC times daily in bolus injections

XX Sequence 8 AA;

XX Query Match 89.6%; Score 43; DB 2; Length 8;
 XX Best Local Similarity 87.5%; Pred. No. 2e+06;
 XX Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 HDAPIGYD 8
 XX |||||
 DB 1 HNAPIGYD 8

RESULT 32

AAW54892
 ID AAW54892 standard; peptide; 8 AA.

XX AAW54892;

XX 24-SEP-1998 (first entry)

XX Isozyme-specific agonist peptide epsilon VI-7.8.

XX epsilon protein kinase C; ischaemic injury; hypoxic exposure.

XX Synthetic.

XX WO9817299-A1.

XX 30-APR-1998.

XX 17-OCT-1997; 97WO-US018716.

XX 18-OCT-1996; 96US-0028724P.

XX (STRD) UNIV LELAND STANFORD JUNIOR.

XX Mochly-Rosen D;

XX WPI; 1998-261181/23.

XX Peptide agonists of protein kinase C - used to reduce ischaemic injury of
 CC cells exposed to hypoxic conditions.

PS Claim 1; Page 32; 47pp; English.

XX The peptides AAW54879-W54901 are agonists of epsilon protein kinase C
CC (PKC). They can be used for reducing ischaemic injury to a cell exposed
CC to hypoxic conditions. They can also be used in a method for identifying
CC a compound effective to induce preconditioning. The peptides are
CC administered at a dose of 1-100 microgram administered once to several
CC times daily in bolus injections

XX Sequence 8 AA;

Query Match 89.6%; Score 43; DB 2; Length 8;
Best Local Similarity 87.5%; Pred. No. 2e+06;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 HDAPIGYD 8
Db 1 HDAPAGYD 8

RESULT 33

ABB99507
ID ABB99507 standard; peptide; 8 AA.

XX ABB99507;

XX 03-MAR-2003 (first entry)

XX Amino acid sequence of a modified pseudo-epsilon RACK peptide.

XX Pseudo-epsilon RACK; RACK; receptor for activated C-kinase;
KM protein kinase C; PKC; tissue damage; ischemia; hypoxia.

XX Synthetic.

XX WO200278600-A2.

XX 10-OCT-2002.

XX 09-NOV-2001; 2001WO-US051600.

XX 10-NOV-2000; 2000US-0247830P.

XX (STRD) UNIV LELAND STANFORD JUNIOR.

XX Mochly-Rosen D;

XX WPI; 2003-092868/08.

XX New composition comprising pseudo-epsilonRACK peptides, useful for
PT treating tissue damage due to ischemia or hypoxia.

XX Claim 6; Page 13; 30pp; English.

XX The present sequence represents a modified pseudo-epsilon RACK
CC octapeptide (see also ABB99501). RACKs (receptors for activated C-kinase)
CC are anchoring molecules, which selectively anchor activated protein
CC kinase C (PKC) isozymes to their respective subcellular sites.
CC Compositions comprising pseudo-epsilon RACK peptides are useful for
CC reducing injury to a cell or tissue exposed to an ischaemic or hypoxic
CC condition. The composition is useful for treating tissue damage due to
CC ischaemia or hypoxia

XX Sequence 8 AA;

Query Match 89.6%; Score 43; DB 6; Length 8;
Best Local Similarity 75.0%; Pred. No. 2e+06;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Oy 1 HDAPIGYD 8
Db 1 HDAPVGYE 8

RESULT 34

ABG76126
ID ABG76126 standard; peptide; 8 AA.

XX ABG76126;

XX 07-MAY-2003 (first entry)

XX Psepsilon RACK peptide #3.

XX Epsilon protein kinase C; epsilonPKC; RACK; ischaemia; hypoxia;
KM receptor for activated C-kinase; myocardial infarction;
KM cardiac ischaemia; psepsilon RACK.

XX Synthetic.

XX US2002168354-A1.

XX 14-NOV-2002.

XX 09-NOV-2001; 2001US-00007363.

XX 10-NOV-2000; 2000US-0247830P.

XX (MOCH/) MOCHLY-ROSEN D.

XX Mochly-Rosen D;

XX WPI; 2003-092868/08.

XX New composition comprising pseudo-epsilonRACK peptides, useful for
PT treating tissue damage due to ischemia or hypoxia.

XX Claim 8; Page 6; 17pp; English.

XX The invention relates to reducing injury to a cell or tissue exposed to
CC an ischaemic or hypoxic condition, comprising administering to the cell
CC or tissue a psepsilon Receptor for Activated C-kinase (RACK) peptide.
CC The RACK peptide is an agonist of epsilon protein kinase C (epsilonPKC).
CC The method is useful in treating or protecting cells and tissues from
CC damage due to an ischaemic or hypoxic event, such as in cardiac ischaemia
CC or myocardial infarction. The present sequence is a psepsilon RACK
CC peptide of the invention

XX Sequence 8 AA;

Query Match 89.6%; Score 43; DB 6; Length 8;
Best Local Similarity 75.0%; Pred. No. 2e+06;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Oy 1 HDAPIGYD 8
Db 1 HDAPVGYE 8

RESULT 35

AEA89933
ID AEA89933 standard; peptide; 8 AA.

XX AEA89933;

XX 08-SEP-2005 (first entry)

XX Receptor for activated C kinase (RACK) peptide #55.

XX Protein interaction; protein kinase C; epsilon-PKC; scleroderma;
KM fibrosis; pulmonary fibrosis; septic shock; ischemia;
KM inflammatory bowel disease; autoimmune disease; multiple sclerosis;
KM Guillain Barre syndrome; psoriasis; Graves disease; rheumatoid arthritis;
KM diabetes mellitus; pulmonary disease;
KM chronic obstructive pulmonary disease; asthma;
KM receptor for activated C kinase; RACK; antiinflammatory; dermatological;

hepatocellular; respiratory-gen.; immunosuppressive; neuroprotective;
KM antiproliferative; CNS-gen.; antithyroid; antitumor; antineoplastic;
KM antidiabetic; antihypertensive; gastrointestinal-gen.; antibacterial;
KM vasotropic; cardiant.

XX Homo sapiens.
OS
PN MO200509124-A2.
PD
PF 30-JUN-2005.
PP
PR 13-DEC-2004; 2004MO-USO41854.
RX
RY 11-DEC-2003; 2003US-0529223P.
ZZ

(STRD) UNIV LEIAND STANFORD JUNIOR.
PA Mochly-Rosen D, Chen LE;
PI WPI; 2005-479333/48.
PS
PT Converting protein kinase C (PKC) agonist peptide to PKC antagonist
PT peptide useful for treating fibrotic or inflammatory disease, involves
PT substituting charged amino acid in agonist peptide with another uncharged
XX amino acid.
XX
XX Claim 8; SEQ ID NO 55; 90pp; English.

The invention relates to a method of converting a protein kinase C (PKC)
CC agonist peptide or peptidomimetic to a PKC antagonist peptide or
CC peptidomimetic, involving substituting at least one amino acid in the
CC agonist peptide or peptidomimetic with an amino acid that converts the
CC PKC agonist peptide or peptidomimetic into a PKC antagonist peptide or
CC peptidomimetic. The invention also relates to a method of inhibiting the
CC activity of a protein kinase C (PKC) enzyme, involving contacting the
CC enzyme with a PKC inhibitor peptide or peptidomimetic, the peptide
CC derived from a PKC agonist peptide or peptidomimetic where at least one
CC amino acid in the agonist peptide or peptidomimetic is substituted with
CC another amino acid sufficient to convert the peptide or peptidomimetic
CC into an antagonist peptide or peptidomimetic. The method is useful for
CC converting a PKC agonist peptide or peptidomimetic to a PKC antagonist
CC peptide or peptidomimetic. The antagonist peptide is useful for treating
CC a disease or condition modulated by epsilon-PKC such as scleroderma,
CC fibrosis or pulmonary fibrosis, septic shock, ischemia, inflammatory,
CC bowel disease, autoimmune disease e.g., multiple sclerosis, Guillain Barre
CC syndrome, psoriasis, Graves disease, rheumatoid arthritis, diabetes
CC mellitus and pulmonary disease e.g., chronic obstructive pulmonary disease
CC and asthma. This sequence represents a receptor for activated C kinase
CC (RACK) peptide used in the method of the invention.

XX Sequence 8 AA:
SQ

Query Match	89.6%	Score 43;	DB 9;	Length 8;					
Best Local Similarity	87.5%;	Pred. No. 2e+06;							
Matches	7;	Conservative	1;	Mismatches	0;	Indels	0;	Gaps	0.

QY 1 HDAPIGYD 8
|:||||||
Db 1 HNAPIGYD 8

RESULT 36
AEA89888
ID AEA89888 standard; peptide; 8 AA.
AC
XX AEA89888;
DT 08-SEP-2005 (first entry)

Receptor for activated C kinase (RACK) peptide #10.
Protein interaction; protein kinase C, epsilon-PKC; scleroderma;
osteoporosis; pulmonary fibrosis; septic shock; ischemia;

OS	Homo sapiens.
XX	
XX	MOZ005059124-A2.
PN	
PD	30-JUN-2005.
XX	
PF	13-DEC-2004; 2004WO-US041854.
XX	
PR	11-DEC-2003; 2003US-0529223P.
XX	
PA	(STRD) UNIV LELAND STANFORD JUNIOR.
PI	Mochly-Rosen D, Chen LE;
DR	WPI; 2005-479333/48.
XX	
PT	Converting protein kinase C (PKC) agonist peptide to PKC antagonist
PT	peptide useful for treating fibrotic or inflammatory diseases, involves
PT	substituting charged amino acid in agonist peptide with another unchanged
PT	amino acid.
PS	
XX	Disclosure; SEQ ID NO 10; 90pp; English.
CC	
XX	The invention relates to a method of converting a protein kinase C (PKC)
CC	agonist peptide or peptidomimetic to a PKC antagonist peptide or
CC	peptidomimetic, involving substituting at least one amino acid in the
CC	agonist peptide or peptidomimetic with an amino acid that converts the
CC	PKC agonist peptide or peptidomimetic into a PKC antagonist peptide or
CC	peptidomimetic. The invention also relates to a method of inhibiting the
CC	activity of a protein kinase C (PKC) enzyme, involving contacting the
CC	enzyme with a PKC inhibitor peptide or peptidomimetic, the peptide
CC	derived from a PKC agonist peptide or peptidomimetic where at least one
CC	amino acid in the agonist peptide or peptidomimetic is substituted with
CC	another amino acid sufficient to convert the peptide or peptidomimetic
CC	into an antagonist peptide or peptidomimetic. The method is useful for
CC	converting a PKC agonist peptide or peptidomimetic to a PKC antagonist
CC	peptide or peptidomimetic. The antagonist peptide is useful for treating
CC	a disease or condition modulated by epsilon-PKC such as scleroderma,
CC	fibrosis or pulmonary fibrosis, septic shock, ischemia, inflammatory
CC	bowel disease, autoimmune disease e.g. multiple sclerosis, Guillain Barre
CC	syndrome, psoriasis, Graves disease, rheumatoid arthritis, diabetes
CC	mellitus and pulmonary disease e.g. chronic obstructive pulmonary disease
CC	and asthma. This sequence represents a receptor for activated C kinase
CC	(RACK) peptide used in the method of the invention.
CC	
CC	
SO	Sequence 8 AA:
Query Match	89.6%; Score 43; DB 9; Length 8;
Best Local Similarity	75.0%; Pred. No. 2e+06;
Matches	6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
OY	1 HDAPGYGD 8
DB	:
	1 HDAPGVGE 8
RESULT 37	
AAW54894	AAW54894 standard; peptide; 8 AA.
XX	
AC	AAW54894;
XX	
DT	24-SEP-1998 (first entry)

XX Isozyme-specific agonist peptide epsilon VI-7.10.
 DE epsilon protein kinase C; ischaemic injury; hypoxic exposure.
 XX
 KM Synthetic.
 OS
 XX WO9817299-A1.
 PN
 XX 30-APR-1998.
 PD
 XX
 XX 17-OCT-1997; 97WO-US018716.
 PF
 XX 18-OCT-1996; 96US-0028724P.
 PR
 XX (STRD) UNIV LELAND STANFORD JUNIOR.
 PA
 XX Mochly-Rosen D;
 PI
 XX WPI; 1998-261181/23.
 DR
 XX
 XX Peptide agonists of protein kinase C - used to reduce ischaemic injury of
 PT cells exposed to hypoxic conditions.
 PS
 XX Claim 1; Page 32; 47pp; English.
 CC The peptides AAW54879-W54901 are agonists of epsilon protein kinase C
 CC (PKC). They can be used for reducing ischaemic injury to a cell exposed
 CC to hypoxic conditions. They can also be used in a method for identifying
 CC a compound effective to induce preconditioning. The peptides are
 CC administered at a dose of 1-100 microgram administered once to several
 CC times daily in bolus injections
 CC
 SQ Sequence 8 AA;
 QY
 DB 1 HDAPIGYD 8
 1 HDAPIAVD 8
 Query Match 87.5%; Score 42; DB 2; Length 8;
 Best Local Similarity 87.5%; Pred. No. 2e+06;
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

RESULT 38
 AAW54895
 ID AAW54895 standard; peptide; 8 AA.
 XX
 XX AAW54895;
 AC
 XX
 XX 24-SEP-1998 (first entry)
 DT
 XX Isozyme-specific agonist peptide epsilon VI-7.11.
 DE
 XX epsilon protein kinase C; ischaemic injury; hypoxic exposure.
 KM
 XX Synthetic.
 OS
 XX WO9817299-A1.
 PN
 XX 30-APR-1998.
 PD
 XX
 XX 17-OCT-1997; 97WO-US018716.
 PF
 XX 18-OCT-1996; 96US-0028724P.
 PR
 XX (STRD) UNIV LELAND STANFORD JUNIOR.
 PA
 XX Mochly-Rosen D;
 PI
 XX WPI; 1998-261181/23.
 DR
 XX
 XX Peptide agonists of protein kinase C - used to reduce ischaemic injury of
 PT

PT cells exposed to hypoxic conditions.
 XX
 XX Claim 1; Page 32; 47pp; English.
 PS
 XX
 CC The peptides AAW54879-W54901 are agonists of epsilon protein kinase C
 CC (PKC). They can be used for reducing ischaemic injury to a cell exposed
 CC to hypoxic conditions. They can also be used in a method for identifying
 CC a compound effective to induce preconditioning. The peptides are
 CC administered at a dose of 1-100 microgram administered once to several
 CC times daily in bolus injections
 CC
 SQ Sequence 8 AA;
 QY
 DB 1 HDAPIGY 7
 1 HDAPIGY 7
 Query Match 87.5%; Score 42; DB 2; Length 8;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 39
 ABB99508
 ID ABB99508 standard; peptide; 8 AA.
 XX
 XX ABB99508;
 AC
 XX 03-MAR-2003 (first entry)
 DT
 XX
 XX Amino acid sequence of a modified pseudo-epsilon RACK peptide.
 DE
 XX Pseudo-epsilon RACK; RACK; receptor for activated C-kinase;
 KM protein kinase C; PKC; tissue damage; ischaemia; hypoxia.
 KW
 XX Synthetic.
 OS
 XX WO200278600-A2.
 PN
 XX 10-OCT-2002.
 PD
 XX
 XX 09-NOV-2001; 2001WO-US051600.
 PF
 XX
 XX 10-NOV-2000; 2000US-0247830P.
 PR
 XX (STRD) UNIV LELAND STANFORD JUNIOR.
 PA
 XX Mochly-Rosen D;
 PI
 XX WPI; 2003-092868/08.
 DR
 XX
 XX New composition comprising pseudo-epsilonRACK peptides, useful for
 PT treating tissue damage due to ischemia or hypoxia.
 PT
 XX
 PS Claim 6; Page 13; 30pp; English.
 CC The present sequence represents a modified pseudo-epsilon RACK
 CC octapeptide (see also ABB99501). RACKs (receptors for activated C-kinase)
 CC are anchoring molecules, which selectively anchor activated protein
 CC kinase C (PKC) isozymes to their respective subcellular sites.
 CC Compositions comprising pseudo-epsilon RACK peptides are useful for
 CC reducing injury to a cell or tissue exposed to an ischaemic or hypoxic
 CC condition. The composition is useful for treating tissue damage due to
 CC ischaemia or hypoxia
 CC
 SQ Sequence 8 AA;
 QY
 DB 1 HDAPIGYD 8
 1 HDAPIGYD 8
 Query Match 87.5%; Score 42; DB 6; Length 8;
 Best Local Similarity 75.0%; Pred. No. 2e+06;
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Db 1 HDAPLGYE 8

RESULT 40

ABG76127
ID ABG76127 standard; peptide; 8 AA.

XX ABG76127;

XX AC
XX DT 07-MAY-2003 (first entry)XX DE
XX psiepsilon RACK peptide #4.XX Epsilon protein kinase C; epsilonPKC; RACK; ischaemia; hypoxia;
KW receptor for activated C-kinase; myocardial infarction;
KW cardiac ischaemia; psiepsilon RACK.

XX OS Synthetic.

XX PN US2002168354-A1.

XX PD 14-NOV-2002.

XX PF 09-NOV-2001; 2001US-00007363.

XX PR 10-NOV-2000; 2000US-0247830P.

XX PA (MOCH/) MOCHLY-ROSEN D.

XX PI Mochly-Rosen D;

XX DR WPI; 2003-092868/08.

XX PT New composition comprising pseudo-epsilonRACK peptides, useful for
XX treating tissue damage due to ischemia or hypoxia.

XX PS Claim 8, Page 6; 17pp; English.

XX CC The invention relates to reducing injury to a cell or tissue exposed to
XX an ischaemic or hypoxic condition, comprising administering to the cell
XX or tissue a psiepsilon Receptor for Activated C-Kinase (RACK) peptide.

XX CC The RACK peptide is an agonist of epsilon protein kinase C (epsilonPKC).

XX CC The method is useful in treating or protecting cells and tissues from
XX damage due to an ischaemic or hypoxic event, such as in cardiac ischaemia
XX or myocardial infarction. The present sequence is a psiepsilon RACK
XX peptide of the invention

XX SQ Sequence 8 AA;

Query Match 87.5%; Score 42; DB 6; Length 8;

Best Local Similarity 75.0%; Pred. No. 2e+06;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;QY 1 HDAPIGYD 8
|||:|:

Db 1 HDAPLGYE 8

Search completed: December 3, 2005, 23:28:01
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OM protein - protein search, using sw model

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Title: US-10-807-553-2
Perfect score: 48
Sequence: 1 HDAPIGVD 8

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

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5: /cgn2_6/ptodata/1/iaa/RE_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	48	100.0	8	US-08-953-033-6	Sequence 6, Appl1
2	48	100.0	156	US-09-771-161A-104	Sequence 104, App
3	48	100.0	737	US-09-772-647-4	Sequence 4, Appl1
4	48	100.0	737	US-10-228-931-4	Sequence 4, Appl1
5	48	100.0	737	US-09-771-161A-195	Sequence 195, App
6	43	89.6	8	US-08-953-033-11	Sequence 11, Appl
7	43	89.6	8	US-08-953-033-14	Sequence 14, Appl
8	42	87.5	8	US-08-953-033-16	Sequence 16, Appl
9	42	87.5	8	US-08-953-033-17	Sequence 17, Appl
10	42	87.5	11	US-08-594-447-19	Sequence 19, Appl
11	42	87.5	11	US-08-541-964-18	Sequence 18, Appl
12	42	87.5	11	US-08-665-647-33	Sequence 33, Appl
13	40	83.3	8	US-08-953-033-9	Sequence 9, Appl1
14	40	83.3	8	US-08-953-033-10	Sequence 10, Appl
15	40	83.3	8	US-08-953-033-12	Sequence 12, Appl
16	40	83.3	8	US-08-953-033-13	Sequence 13, Appl
17	39	81.2	8	US-08-953-033-15	Sequence 15, Appl
18	38	79.2	8	US-08-953-033-20	Sequence 20, Appl
19	38	79.2	682	US-09-538-092-1003	Sequence 1003, Ap
20	38	79.2	739	US-09-949-016-7606	Sequence 7606, Ap
21	37.5	78.1	14	US-08-953-033-23	Sequence 23, Appl
22	35	72.9	8	US-08-953-033-8	Sequence 8, Appl1
23	35	72.9	6	US-08-953-033-7	Sequence 7, Appl1
24	35	72.9	14	US-09-747-287A-207	Sequence 207, App
25	35	72.9	14	US-09-394-019C-156	Sequence 156, App
26	35	72.9	14	US-09-394-019C-253	Sequence 253, App
27	35	72.9	14	US-09-394-019C-401	Sequence 401, App

28	72.9	361	2	US-09-949-016-11594	Sequence 11594, A
29	72.9	374	2	US-09-489-039A-7383	Sequence 7383, Ap
30	72.9	400	2	US-09-252-991A-26250	Sequence 26250, A
31	72.9	649	2	US-09-134-001C-3891	Sequence 3891, Ap
32	70.8	10	1	US-08-584-226-22	Sequence 22, Appl
33	70.8	16	2	US-09-747-287A-91	Sequence 91, Appl
34	70.8	16	2	US-09-747-287A-92	Sequence 92, Appl
35	70.8	16	2	US-09-747-287A-93	Sequence 93, Appl
36	70.8	16	2	US-09-747-287A-206	Sequence 206, App
37	70.8	18	2	US-09-747-287A-94	Sequence 94, Appl
38	70.8	18	2	US-09-747-287A-95	Sequence 95, Appl
39	70.8	18	2	US-09-747-287A-96	Sequence 96, Appl
40	70.8	18	2	US-09-747-287A-97	Sequence 97, Appl
41	70.8	18	2	US-09-747-287A-98	Sequence 98, Appl
42	70.8	18	2	US-09-747-287A-99	Sequence 99, Appl
43	70.8	18	2	US-09-747-287A-204	Sequence 204, App
44	70.8	153	2	US-09-270-767-34573	Sequence 34573, A
45	70.8	153	2	US-09-270-767-49790	Sequence 49790, A
46	70.8	245	2	US-09-902-540-13549	Sequence 13549, A
47	70.8	340	2	US-09-270-767-58348	Sequence 58348, A
48	70.8	477	2	US-09-270-767-43020	Sequence 43020, A
49	70.8	483	2	US-09-543-681A-5752	Sequence 5752, Ap
50	70.8	500	2	US-09-325-932A-149	Sequence 149, App
51	70.8	554	2	US-09-198-452A-140	Sequence 140, App
52	70.8	554	2	US-09-438-185A-124	Sequence 124, App
53	70.8	659	2	US-09-392-772-10	Sequence 10, Appl
54	70.8	680	2	US-09-252-991A-17566	Sequence 17566, A
55	70.8	683	2	US-09-543-681A-5403	Sequence 5403, Ap
56	70.8	703	2	US-09-902-540-10686	Sequence 10686, A
57	70.8	716	2	US-09-489-039A-8243	Sequence 8243, Ap
58	70.8	730	2	US-09-328-352-4765	Sequence 4765, Ap
59	70.8	1131	2	US-09-487-5588-72	Sequence 72, Appl
60	68.8	252	1	US-08-602-359A-35	Sequence 35, Appl
61	68.8	486	2	US-09-489-039A-7965	Sequence 7965, Ap
62	68.8	690	2	US-09-540-236-3507	Sequence 26, Appl
63	66.7	11	1	US-08-594-447-26	Sequence 26, Appl
64	66.7	11	1	US-08-541-964-25	Sequence 25, Appl
65	66.7	11	1	US-08-665-647-40	Sequence 40, Appl
66	66.7	102	1	US-07-901-703-5	Sequence 5, Appl1
67	66.7	102	1	US-08-278-729A-11	Sequence 11, Appl
68	66.7	102	1	US-08-155-343A-11	Sequence 11, Appl
69	66.7	102	1	US-08-406-672-11	Sequence 11, Appl
70	66.7	102	1	US-08-335-583C-50	Sequence 50, Appl
71	66.7	102	1	US-08-643-563A-11	Sequence 11, Appl
72	66.7	102	1	US-08-643-763A-11	Sequence 11, Appl
73	66.7	102	1	US-08-462-623-11	Sequence 11, Appl
74	66.7	102	1	US-08-451-953A-11	Sequence 11, Appl
75	66.7	102	1	US-08-445-668A-11	Sequence 11, Appl
76	66.7	102	1	US-08-461-397A-11	Sequence 11, Appl
77	66.7	102	1	US-08-912-088-11	Sequence 11, Appl
78	66.7	102	2	US-08-278-730A-11	Sequence 11, Appl
79	66.7	102	2	US-08-478-097A-6	Sequence 6, Appl1
80	66.7	102	2	US-08-445-467-11	Sequence 11, Appl
81	66.7	102	2	US-08-480-515A-11	Sequence 11, Appl
82	66.7	102	2	US-08-414-033A-11	Sequence 11, Appl
83	66.7	102	2	US-08-271-556A-9	Sequence 9, Appl1
84	66.7	102	2	US-08-931-858E-158	Sequence 158, App
85	66.7	102	2	US-08-981-739-158	Sequence 158, App
86	66.7	102	2	US-08-440-894A-11	Sequence 11, Appl
87	66.7	102	2	US-09-170-936-11	Sequence 11, Appl
88	66.7	102	2	US-08-461-113-11	Sequence 11, Appl
89	66.7	102	2	US-09-128-026-158	Sequence 158, App
90	66.7	102	2	US-09-486-398-6	Sequence 6, Appl1
91	66.7	102	2	US-08-456-033-11	Sequence 11, Appl
92	66.7	102	2	US-08-643-321-10	Sequence 10, Appl
93	66.7	102	2	US-09-464-206-11	Sequence 11, Appl
94	66.7	102	2	US-08-404-616A-11	Sequence 11, Appl
95	66.7	102	2	US-09-230-616-158	Sequence 158, App
96	66.7	102	2	US-09-374-958C-45	Sequence 45, Appl
97	66.7	102	2	US-09-220-527-158	Sequence 158, App
98	66.7	102	2	US-09-220-527-158	Sequence 158, App
99	66.7	102	2	US-08-260-675-11	Sequence 11, Appl
100	66.7	102	2	US-09-374-936-45	Sequence 45, Appl

ALIGNMENTS

RESULT 1
US-08-953-033-6
Sequence 6, Application US/08953033
Patent No. 6165977
GENERAL INFORMATION:
APPLICANT: Mochly-Rosen, Daria
TITLE OF INVENTION: ISOZYME-SPECIFIC ACTIVATORS
TITLE OF INVENTION: OF PROTEIN KINASE C - METHODS AND COM
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESS: Dellinger & Associates
STREET: 350 Cambridge Ave., Suite 250
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/953,033
FILING DATE: 17-OCT-1997
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/028,724
FILING DATE: 18-OCT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Pettibory, Joanne R.
REGISTRATION NUMBER: 42,995
REFERENCE/DOCKET NUMBER: 8600-0174.30
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-324-0880
TELEFAX: 650-324-0960
TELEX:
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
STRANDNESS: single
TOPOLOGY: linear
MOLSCULE TYPE: peptide
FEATURE:
NAME/KEY: Other
LOCATION: 1...8
OTHER INFORMATION: epsilon-PKC residues 85-92; epsilonV1-7; E7
US-08-953-033-6

Query Match 100.0%; Score 48; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HDAPIGYD 8
|||||
Db 1 HDAPIGYD 8

RESULT 2
US-09-771-161A-104
Sequence 104, Application US/09771161A
Patent No. 6936450
GENERAL INFORMATION:
APPLICANT: LEVINE, et al.
TITLE OF INVENTION: VARIANTS OF PROTEIN KINASES
FILE REFERENCE: 802620-2005.1
CURRENT APPLICATION NUMBER: US/09/771,161A

CURRENT FILING DATE: 2001-01-26
PRIOR APPLICATION NUMBER: 09/724,676
PRIOR FILING DATE: 2000-11-28
PRIOR APPLICATION NUMBER: 136776
PRIOR FILING DATE: 2000-06-15
PRIOR APPLICATION NUMBER: 135619
PRIOR FILING DATE: 2000-04-12
NUMBER OF SEQ ID NOS: 273
SOFTWARE: PatentIn version 3.0
SEQ ID NO 104
LENGTH: 156
TYPE: PRT
ORGANISM: Homo sapiens
US-09-771-161A-104

Query Match 100.0%; Score 48; DB 2; Length 156;
Best Local Similarity 100.0%; Pred. No. 0.095;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HDAPIGYD 8
|||||
Db 85 HDAPIGYD 92

RESULT 3
US-09-772-647-4
Sequence 4, Application US/09772647
Patent No. 6521815
GENERAL INFORMATION:
APPLICANT: Verma, Ajit K
APPLICANT: Reddig, Peter J
TITLE OF INVENTION: Animal Model System for Squamous Cell Carcinoma
FILE REFERENCE: 960296.97613
CURRENT APPLICATION NUMBER: US/09/772,647
CURRENT FILING DATE: 2001-01-30
NUMBER OF SEQ ID NOS: 6
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 4
LENGTH: 737
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURES:
OTHER INFORMATION: Description of Artificial Sequence: T7 tag and
OTHER INFORMATION: mouse protein kinase C epsilon coding sequence
US-09-772-647-4

Query Match 100.0%; Score 48; DB 2; Length 737;
Best Local Similarity 100.0%; Pred. No. 0.48; 0; Indels 0; Gaps 0;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HDAPIGYD 8
|||||
Db 85 HDAPIGYD 92

RESULT 4
US-10-228-931-4
Sequence 4, Application US/10228931
Patent No. 6897352
GENERAL INFORMATION:
APPLICANT: Verma, Ajit K
APPLICANT: Reddig, Peter J
APPLICANT: Jansen, Aaron P
TITLE OF INVENTION: Animal Model System for Squamous Cell Carcinoma
FILE REFERENCE: 960296.97613
CURRENT APPLICATION NUMBER: US/10/228,931
CURRENT FILING DATE: 2002-08-27
PRIOR APPLICATION NUMBER: US/09/772,647
PRIOR FILING DATE: 2001-01-30
NUMBER OF SEQ ID NOS: 6
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 4

LENGTH: 737
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: T7 tag and
OTHER INFORMATION: mouse protein Kinase C epsilon coding sequence
US-10-228-931-4

Query Match 100.0%; Score 48; DB 2; Length 737;
Best Local Similarity 100.0%; Pred. No. 0.48;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HDAPIGYD 8
Db 85 HDAPIGYD 92

RESULT 5
US-09-771-161A-195
Sequence 195, Application US/09771161A
Patent No. 6936450
GENERAL INFORMATION:
APPLICANT: LEVINE, et al.
TITLE OF INVENTION: VARIANTS OF PROTEIN KINASES
FILE REFERENCE: 802620-2005.1
CURRENT APPLICATION NUMBER: US/09/771,161A
CURRENT FILING DATE: 2001-01-26
PRIOR APPLICATION NUMBER: 09/724,676
PRIOR FILING DATE: 2000-11-28
PRIOR APPLICATION NUMBER: 136776
PRIOR FILING DATE: 2000-06-15
PRIOR APPLICATION NUMBER: 135619
PRIOR FILING DATE: 2000-04-12
NUMBER OF SEQ ID NOS: 273
SOFTWARE: PatentIn version 3.0
SEQ ID NO 195
LENGTH: 737
TYPE: PRT
ORGANISM: Homo sapiens
US-09-771-161A-195

Query Match 100.0%; Score 48; DB 2; Length 737;
Best Local Similarity 100.0%; Pred. No. 0.48;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HDAPIGYD 8
Db 85 HDAPIGYD 92

RESULT 6
US-08-953-033-11
Sequence 11, Application US/08953033
Patent No. 6165977
GENERAL INFORMATION:
APPLICANT: Mochly-Rosen, Daria
TITLE OF INVENTION: ISOZYME-SPECIFIC ACTIVATORS
TITLE OF INVENTION: OF PROTEIN KINASE C - METHODS AND COM
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dehlinger & Associates
STREET: 350 Cambridge Ave., Suite 250
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/953,033
FILING DATE: 17-OCT-1997
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/028,724
FILING DATE: 18-OCT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Petithory, Joanne R.
REGISTRATION NUMBER: 42,995
REFERENCE/DOCKET NUMBER: 8600-0174.30
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-324-0880
TELEFAX: 650-324-0960
TELEX:
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Other
LOCATION: 1...8
OTHER INFORMATION: epsilonVI-7.5
US-08-953-033-11

Query Match 89.6%; Score 43; DB 2; Length 8;
Best Local Similarity 87.5%; Pred. No. 4.6e+05;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HDAPIGYD 8
Db 1 HMAPIGYD 8

RESULT 7
US-08-963-033-14
Sequence 14, Application US/08953033
Patent No. 6165977
GENERAL INFORMATION:
APPLICANT: Mochly-Rosen, Daria
TITLE OF INVENTION: ISOZYME-SPECIFIC ACTIVATORS
TITLE OF INVENTION: OF PROTEIN KINASE C - METHODS AND COM
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dehlinger & Associates
STREET: 350 Cambridge Ave., Suite 250
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/953,033
FILING DATE: 17-OCT-1997
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/028,724
FILING DATE: 18-OCT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Petithory, Joanne R.
REGISTRATION NUMBER: 42,995
REFERENCE/DOCKET NUMBER: 8600-0174.30
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-324-0880
TELEFAX: 650-324-0960
TELEX:

;; INFORMATION FOR SEQ ID NO: 14:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 8 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
;; FEATURES:
;; NAME/KEY: Other
;; LOCATION: 1...8
;; OTHER INFORMATION: epsilononv1-7.8
US-08-953-033-14

Query Match 89.6%; Score 43; DB 2; Length 8;
Best Local Similarity 87.5%; Pred. No. 4.6e+05;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 HDAPIGYD 8
Db 1 HDAPAGYD 8

RESULT 8
US-08-953-033-16
Sequence 16, Application US/08953033
Patent No. 6165977
GENERAL INFORMATION:
APPLICANT: Mochly-Rosen, Daria
TITLE OF INVENTION: ISOZYME-SPECIFIC ACTIVATORS
TITLE OF INVENTION: OF PROTEIN KINASE C - METHODS AND COM
NUMBER OF INVENTION: POSITIONS
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Delinger & Associates
STREET: 350 Cambridge Ave., Suite 250
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/953,033
FILING DATE: 17-OCT-1997
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/028,724
FILING DATE: 18-OCT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Pelichory, Joanne R.
REGISTRATION NUMBER: 42,995
REFERENCE/DOCKET NUMBER: 8600-0174.30
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-324-0880
TELEFAX: 650-324-0960
TELEX:
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURES:
NAME/KEY: No. 6165977e
LOCATION: 1...8
OTHER INFORMATION: epsilononv1-7.10
-033-16

Best Local Similarity 87.5%; Pred. No. 4.6e+05;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 HDAPIGYD 8
Db 1 HDAPAGYD 8

RESULT 9
US-08-953-033-17
Sequence 17, Application US/08953033
Patent No. 6165977
GENERAL INFORMATION:
APPLICANT: Mochly-Rosen, Daria
TITLE OF INVENTION: ISOZYME-SPECIFIC ACTIVATORS
TITLE OF INVENTION: OF PROTEIN KINASE C - METHODS AND COM
NUMBER OF INVENTION: POSITIONS
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Delinger & Associates
STREET: 350 Cambridge Ave., Suite 250
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/953,033
FILING DATE: 17-OCT-1997
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/028,724
FILING DATE: 18-OCT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Pelichory, Joanne R.
REGISTRATION NUMBER: 42,995
REFERENCE/DOCKET NUMBER: 8600-0174.30
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-324-0880
TELEFAX: 650-324-0960
TELEX:
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURES:
NAME/KEY: No. 6165977e
LOCATION: 1...8
OTHER INFORMATION: epsilononv1-7.11
US-08-953-033-17

Query Match 87.5%; Score 42; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HDAPIGY 7
Db 1 HDAPIGY 7

RESULT 10
US-08-594-447-19
Sequence 19, Application US/08594447
Patent No. 5776716
GENERAL INFORMATION:
APPLICANT: Ron, Dorit

APPLICANT: Napolitano, Eugene W.
APPLICANT: Voronova, Anna F.
TITLE OF INVENTION: METHODS FOR IDENTIFYING AGENTS WHICH
BLOCK THE INTERACTION OF FYN WITH PKC-THETA, AND USES
TITLE OF INVENTION: THEREOF
NUMBER OF SEQUENCES: 75
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 2000 Pennsylvania Avenue, NW - Ste. 5500
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20006-1888
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/594,447
FILING DATE: 31-JAN-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Murashige, Kate H.
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 22550-20025.24
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-1500
TELEFAX: (202) 822-0168
TELEX: 90-4030 MRSNFOERSWSH
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Peptide
LOCATION: 1..11
OTHER INFORMATION: /label= epsilon-VI-3
US-08-594-447-19
Query Match 87.5%; Score 42; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.083;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 HDAPIGY 7
Db 5 HDAPIGY 11
RESULT 11
US-08-541-964-18
Sequence 18, Application US/08541964
Patent No. 5783405
GENERAL INFORMATION:
APPLICANT: Mochly-Rosen, Daria
APPLICANT: Ron, Dorit
APPLICANT: Kavaar, Lawrence W.
APPLICANT: Napolitano, Eugene W.
TITLE OF INVENTION: A RAPID SCREENING METHOD FOR EFFECTORS
NUMBER OF SEQUENCES: 74
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 2000 PENNSYLVANIA AVENUE, NW-STE. 5500
CITY: WASHINGTON
STATE: DC
COUNTRY: USA
ZIP: 20006-1888
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/541,964
FILING DATE: 10-OCT-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Murashige, Kate H.
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 22550-20025.23
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-1500
TELEFAX: (202) 822-0168
TELEX: 90-4030 MRSNFOERSWSH
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Peptide
LOCATION: 1..11
OTHER INFORMATION: /label= epsilon-VI-3
US-08-541-964-18
Query Match 87.5%; Score 42; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.083;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 HDAPIGY 7
Db 5 HDAPIGY 11
RESULT 12
US-08-665-647-33
Sequence 33, Application US/08665647
Patent No. 5935803
GENERAL INFORMATION:
APPLICANT: Dasquez, Nicki J.
APPLICANT: Ron, Dorit
APPLICANT: Voronova, Anna F.
APPLICANT: Napolitano, Eugene W.
TITLE OF INVENTION: METHODS TO IDENTIFY IMMUNOMODULATORS
USING COGNATE INTERACTION OF PKC-THETA
NUMBER OF SEQUENCES: 89
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 2000 Pennsylvania Avenue, NW - Ste. 5500
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20006-1888
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/665,647
FILING DATE: 18-JUN-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Murashige, Kate H.
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 22550-20025.25
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-1500
TELEFAX: (202) 822-0168
TELEX: 90-4030 MRSNFOERSWSH

INFORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Peptide
LOCATION: 1...11
OTHER INFORMATION: /label= epsilon-VI-3
US-08-665-647-33

Query Match 87.5%; Score 42; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.063;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HDAPIGY 7
Db 5 HDAPIGY 11

RESULT 13
US-08-953-033-9
Sequence 9, Application US/08953033
Patent No. 6165977
GENERAL INFORMATION:
APPLICANT: Mochly-Rosen, Daria
TITLE OF INVENTION: ISOZYME-SPECIFIC ACTIVATORS
TITLE OF INVENTION: OF PROTEIN KINASE C - METHODS AND COM
POSITIONS
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESS: Dehlinger & Associates
STREET: 350 Cambridge Ave., Suite 250
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/953.033
FILING DATE: 17-OCT-1997
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/028,724
FILING DATE: 18-OCT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Pelichory, Joanne R.
REGISTRATION NUMBER: 42,995
REFERENCE/DOCKET NUMBER: 8600-0174.30
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-324-0880
TELEFAX: 650-324-0960
TELEX:
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Other
LOCATION: 1...8
OTHER INFORMATION: epsilonVI-7.3
US-08-953-033-9

Query Match 83.3%; Score 40; DB 2; Length 8;

Best Local Similarity 87.5%; Pred. No. 4.6e+05;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 HDAPIGYD 8
Db 1 HDAPIGYD 8

RESULT 14
US-08-953-033-10
Sequence 10, Application US/08953033
Patent No. 6165977
GENERAL INFORMATION:
APPLICANT: Mochly-Rosen, Daria
TITLE OF INVENTION: ISOZYME-SPECIFIC ACTIVATORS
TITLE OF INVENTION: OF PROTEIN KINASE C - METHODS AND COM
POSITIONS
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESS: Dehlinger & Associates
STREET: 350 Cambridge Ave., Suite 250
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/953.033
FILING DATE: 17-OCT-1997
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/028,724
FILING DATE: 18-OCT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Pelichory, Joanne R.
REGISTRATION NUMBER: 42,995
REFERENCE/DOCKET NUMBER: 8600-0174.30
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-324-0880
TELEFAX: 650-324-0960
TELEX:
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Other
LOCATION: 1...8
OTHER INFORMATION: epsilonVI-7.4
US-08-953-033-10

Query Match 83.3%; Score 40; DB 2; Length 8;
Best Local Similarity 87.5%; Pred. No. 4.6e+05;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 HDAPIGYD 8
Db 1 HDAPIGYD 8

RESULT 15
US-08-953-033-12
Sequence 12, Application US/08953033
Patent No. 6165977
GENERAL INFORMATION:
APPLICANT: Mochly-Rosen, Daria

TITLE OF INVENTION: ISOZYME-SPECIFIC ACTIVATORS
TITLE OF INVENTION: OF PROTEIN KINASE C - METHODS AND COM
TITLE OF INVENTION: POSITIONS
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dehlinger & Associates
STREET: 350 Cambridge Ave., Suite 250
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/953,033
FILING DATE: 17-OCT-1997
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/028,724
FILING DATE: 18-OCT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Petithory, Joanne R.
REGISTRATION NUMBER: 42,995
REFERENCE/DOCKET NUMBER: 8600-0174.30
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-324-0880
TELEFAX: 650-324-0960
TELEX:
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Other
LOCATION: 1...8
OTHER INFORMATION: epsilonV1-7.6
US-08-953-033-12

Query Match 83.3%; Score 40; DB 2; Length 8;
Best Local Similarity 87.5%; Pred. No. 4.6e+05;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 HDAPIGVD 8
Db 1 HAAPIGVD 8

RESULT 16
US-08-953-033-13
Sequence 13, Application US/08953033
Patent No. 6165977
GENERAL INFORMATION:
APPLICANT: Mochly-Rosen, Daria
TITLE OF INVENTION: ISOZYME-SPECIFIC ACTIVATORS
TITLE OF INVENTION: OF PROTEIN KINASE C - METHODS AND COM
TITLE OF INVENTION: POSITIONS
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dehlinger & Associates
STREET: 350 Cambridge Ave., Suite 250
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/953,033
FILING DATE: 17-OCT-1997
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/028,724
FILING DATE: 18-OCT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Petithory, Joanne R.
REGISTRATION NUMBER: 42,995
REFERENCE/DOCKET NUMBER: 8600-0174.30
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-324-0880
TELEFAX: 650-324-0960
TELEX:
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Other
LOCATION: 1...8
OTHER INFORMATION: epsilonV1-7.7
US-08-953-033-13

Query Match 83.3%; Score 40; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DAPIGVD 8
Db 2 DAPIGVD 8

RESULT 17
US-08-953-033-15
Sequence 15, Application US/08953033
Patent No. 6165977
GENERAL INFORMATION:
APPLICANT: Mochly-Rosen, Daria
TITLE OF INVENTION: ISOZYME-SPECIFIC ACTIVATORS
TITLE OF INVENTION: OF PROTEIN KINASE C - METHODS AND COM
TITLE OF INVENTION: POSITIONS
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dehlinger & Associates
STREET: 350 Cambridge Ave., Suite 250
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/953,033
FILING DATE: 17-OCT-1997
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/028,724
FILING DATE: 18-OCT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Petithory, Joanne R.
REGISTRATION NUMBER: 42,995
REFERENCE/DOCKET NUMBER: 8600-0174.30
TELECOMMUNICATION INFORMATION:

TELEPHONE: 650-324-0880
TELEFAX: 650-324-0960
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Other
LOCATION: 1...8
OTHER INFORMATION: epsilonV1-7.9
US-08-953-033-15

Query Match 81.2% Score 39; DB 2; Length 8;
Best Local Similarity 87.5%; Pred. No. 4.6e+05;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 HDAPIGYD 8
Db 1 HDAPIGAD 8

RESULT 18
US-08-953-033-20
Sequence 20, Application US/08953033
Patent No. 6165977
GENERAL INFORMATION:
APPLICANT: Mochly-Rosen, Daria
TITLE OF INVENTION: ISOZYME-SPECIFIC ACTIVATORS
TITLE OF INVENTION: OF PROTEIN KINASE C - METHODS AND COM
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSER: Dehlinger & Associates
STREET: 350 Cambridge Ave., Suite 250
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/953.033
FILING DATE: 17-OCT-1997
CLASSIFICATION: 530
PRIOR APPLICATION NUMBER: 60/028,724
APPLICATION DATA:
FILING DATE: 18-OCT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Petichory, Joanne R.
REGISTRATION NUMBER: 42,995
REFERENCE/DOCKET NUMBER: 8600-0174.30
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-324-0880
TELEFAX: 650-324-0960
TELEX:
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Other
LOCATION: 1...8
OTHER INFORMATION: nV1-7

US-08-953-033-20

Query Match 79.2% Score 38; DB 2; Length 8;
Best Local Similarity 62.5%; Pred. No. 4.6e+05;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 HDAPIGYD 8
Db 1 HETPLGYD 8

RESULT 19
US-09-538-092-1003
Sequence 1003, Application US/09538092
Patent No. 675314
GENERAL INFORMATION:
APPLICANT: Glot, Loic
APPLICANT: Mansfield, Traci A.
TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same
FILE REFERENCE: 15966-542
CURRENT APPLICATION NUMBER: US/09/538.092
CURRENT FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: 60/127,352
PRIOR FILING DATE: 1999-04-01
PRIOR APPLICATION NUMBER: 60/178,965
PRIOR FILING DATE: 2000-02-01
NUMBER OF SEQ ID NOS: 1387
SOFTWARE: CurpatSeqFormatter Version 0.9
SEQ ID NO 1003
LENGTH: 682
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: (0)...(0)
OTHER INFORMATION: Polypeptide Accession Number P24723
US-09-538-092-1003

Query Match 79.2% Score 38; DB 2; Length 682;
Best Local Similarity 62.5%; Pred. No. 37;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 HDAPIGYD 8
Db 88 HETPLGYD 95

RESULT 20
US-09-949-016-7606
Sequence 7606, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: C0001307
CURRENT APPLICATION NUMBER: US/09/949.016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 7606
LENGTH: 739
TYPE: PRT
ORGANISM: Human
US-09-949-016-7606

Query Match 79.2% Score 38; DB 2; Length 739;

Best Local Similarity 62.5%; Pred. No. 40;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 1 HDAPIGVD 8
Db 144 HETPLGVD 151

RESULT 21

US-08-953-033-23
; Sequence 23, Application US/08953033
; Patent No. 6165977
; GENERAL INFORMATION:
; APPLICANT: Mochly-Rosen, Daria
; TITLE OF INVENTION: ISOZYME-SPECIFIC ACTIVATORS
; TITLE OF INVENTION: OF PROTEIN KINASE C - METHODS AND COM
; NUMBER OF INVENTION: POSITIONS
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dehlinger & Associates
; STREET: 350 Cambridge Ave., Suite 250
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/953,033
; FILING DATE: 17-OCT-1997
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/028,724
; FILING DATE: 18-OCT-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Petithory, Joanne R.
; REGISTRATION NUMBER: 42,995
; REFERENCE/DOCKET NUMBER: 8600-0174.30
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-324-0880
; TELEFAX: 650-324-0960
; TELEX:
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Other
; LOCATION: 1...14
; OTHER INFORMATION: epsilonV1-7.1x
US-08-953-033-23

Query Match 78.1%; Score 37.5; DB 2; Length 14;
Best Local Similarity 88.9%; Pred. No. 0.78;
Matches 8; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 HDAPIGVD 8
Db 4 HDAPIGVD 12

RESULT 22

US-08-953-033-8
; Sequence 8, Application US/08953033
; Patent No. 6165977
; GENERAL INFORMATION:
; APPLICANT: Mochly-Rosen, Daria

; TITLE OF INVENTION: ISOZYME-SPECIFIC ACTIVATORS
; TITLE OF INVENTION: OF PROTEIN KINASE C - METHODS AND COM
; TITLE OF INVENTION: POSITIONS
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dehlinger & Associates
; STREET: 350 Cambridge Ave., Suite 250
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/953,033
; FILING DATE: 17-OCT-1997
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/028,724
; FILING DATE: 18-OCT-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Petithory, Joanne R.
; REGISTRATION NUMBER: 42,995
; REFERENCE/DOCKET NUMBER: 8600-0174.30
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-324-0880
; TELEFAX: 650-324-0960
; TELEX:
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Other
; LOCATION: 1...6
; OTHER INFORMATION: epsilonV1-7.2
US-08-953-033-8

Query Match 72.9%; Score 35; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HDAPIG 6
Db 1 HDAPIG 6

RESULT 23

US-08-953-033-7
; Sequence 7, Application US/08953033
; Patent No. 6165977
; GENERAL INFORMATION:
; APPLICANT: Mochly-Rosen, Daria
; TITLE OF INVENTION: ISOZYME-SPECIFIC ACTIVATORS
; TITLE OF INVENTION: OF PROTEIN KINASE C - METHODS AND COM
; NUMBER OF INVENTION: POSITIONS
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dehlinger & Associates
; STREET: 350 Cambridge Ave., Suite 250
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/953,033
FILING DATE: 17-OCT-1997
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/028,724
FILING DATE: 18-OCT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Petithory, Joanne R.
REGISTRATION NUMBER: 42,995
REFERENCE/DOCKET NUMBER: 8600-0174.30
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-324-0880
TELEFAX: 650-324-0960
TELEX:
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Other
LOCATION: 1...8
OTHER INFORMATION: epsilonV1-7.1
US-08-953-033-7

Query Match 72.9%; Score 35; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HDAPIG 6
Db 1 HDAPIG 6

RESULT 24
US-09-747-287A-207
Sequence 207, Application US/09747287A
Patent No. 6893868
GENERAL INFORMATION:
APPLICANT: KOMORIYA, AKIRA
APPLICANT: PACKARD, BEVERLY S.
TITLE OF INVENTION: HOMO-DOUBLY LABELED COMPOSITIONS FOR THE DETECTION OF ENZYME
FILE REFERENCE: 300-948600US
CURRENT FILING DATE: 2000-12-22
PRIOR FILING DATE: 1999-09-10
PRIOR APPLICATION NUMBER: US 09/349,019
PRIOR FILING DATE: 1999-09-10
PRIOR APPLICATION NUMBER: US08/802,981
PRIOR FILING DATE: 1997-02-20
PRIOR APPLICATION NUMBER: PCT/US00/24882
PRIOR FILING DATE: 2000-09-11
NUMBER OF SEQ ID NOS: 246
SOFTWARE: PatentIn version 3.3
SEQ ID NO 207
LENGTH: 14
TYPE: PRT
ORGANISM: Artificial
FEATURE:
OTHER INFORMATION: Synthetic peptide.
FEATURE:
NAME/KEY: misc_feature
LOCATION: (4)..(4)
OTHER INFORMATION: Xaa is epsilon-aminoacaproic acid
US-09-747-287A-207

Query Match 72.9%; Score 35; DB 2; Length 14;
Best Local Similarity 85.7%; Pred. No. 2.4;

Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 HDAPIG 7
Db 8 HDAPKGY 14

RESULT 25
US-09-394-019C-156
Sequence 156, Application US/09394019C
Patent No. 6936687
GENERAL INFORMATION:
APPLICANT: OncoImmunin, Inc.
APPLICANT: Komoriya, Akira
APPLICANT: Packard, Beverly
TITLE OF INVENTION: COMPOSITIONS FOR THE DETECTION OF ENZYME ACTIVITY IN BIOLOGICAL
FILE REFERENCE: 300-903820US
CURRENT FILING DATE: 1999-09-10
PRIOR FILING DATE: 1998-02-20
PRIOR APPLICATION NUMBER: PCT/US98/00300
PRIOR FILING DATE: 1997-02-20
PRIOR APPLICATION NUMBER: US 08/802,981
NUMBER OF SEQ ID NOS: 405
SOFTWARE: PatentIn version 3.2
SEQ ID NO 156
LENGTH: 14
TYPE: PRT
ORGANISM: Artificial
FEATURE:
OTHER INFORMATION: Synthetic peptide substrate
FEATURE:
NAME/KEY: MOD_RES
LOCATION: (1)-(1)
OTHER INFORMATION: K is blocked with Fmoc
FEATURE:
NAME/KEY: MOD_RES
LOCATION: (4)..(4)
OTHER INFORMATION: X is epsilon aminoacaproic acid
US-09-394-019C-156

Query Match 72.9%; Score 35; DB 2; Length 14;
Best Local Similarity 85.7%; Pred. No. 2.4;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 HDAPIGY 7
Db 8 HDAPKGY 14

RESULT 26
US-09-394-019C-253
Sequence 253, Application US/09394019C
Patent No. 6936687
GENERAL INFORMATION:
APPLICANT: OncoImmunin, Inc.
APPLICANT: Komoriya, Akira
APPLICANT: Packard, Beverly
TITLE OF INVENTION: COMPOSITIONS FOR THE DETECTION OF ENZYME ACTIVITY IN BIOLOGICAL
FILE REFERENCE: 300-903820US
CURRENT FILING DATE: 1999-09-10
PRIOR FILING DATE: 1998-02-20
PRIOR APPLICATION NUMBER: PCT/US98/00300
PRIOR FILING DATE: 1997-02-20
PRIOR APPLICATION NUMBER: US 08/802,981
NUMBER OF SEQ ID NOS: 405

SOFTWARE: Patentin version 3.2
; SEQ ID NO 253
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Synthetic peptide substrate
; NAME/KEY: MOD_RES
; LOCATION: (4)..(4)
; OTHER INFORMATION: X is epsilon-aminocaproic acid
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (4)..(4)
; OTHER INFORMATION: Xaa can be any naturally occurring amino acid
US-09-394-019C-253

Query Match 72.9%; Score 35; DB 2; Length 14;
Best Local Similarity 85.7%; Pred. No. 2.4;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 HDAPIGY 7
Db 8 HDAPKGY 14

RESULT 27
US-09-394-019C-401
; Sequence 401, Application US/09394019C
; Patent No. 6936687
; GENERAL INFORMATION:
; APPLICANT: Oncolimmun, Inc.
; APPLICANT: Komoriya, Akira
; TITLE OF INVENTION: COMPOSITIONS FOR THE DETECTION OF ENZYME ACTIVITY IN BIOLOGICAL
; FILE REFERENCE: 300-903820US
; CURRENT APPLICATION NUMBER: US/09/394,019C
; CURRENT FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: PCT/US98/00300
; PRIOR FILING DATE: 1998-02-20
; PRIOR APPLICATION NUMBER: US 08/802,981
; PRIOR FILING DATE: 1997-02-20
; NUMBER OF SEQ ID NOS: 405
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 401
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Synthetic peptide. Chemically synthesized protease substrate.
; NAME/KEY: misc_feature
; LOCATION: (4)..(4)
; OTHER INFORMATION: Xaa is epsilon-aminocaproic acid
US-09-394-019C-401

Query Match 72.9%; Score 35; DB 2; Length 14;
Best Local Similarity 85.7%; Pred. No. 2.4;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 HDAPIGY 7
Db 8 HDAPKGY 14

RESULT 28
US-09-949-016-11594
; Sequence 11594, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CLO01307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14,755
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11594
; LENGTH: 361
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-11594

Query Match 72.9%; Score 35; DB 2; Length 361;
Best Local Similarity 75.0%; Pred. No. 71;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 HDAPIGYD 8
Db 100 HDIPIGID 107

RESULT 29
US-09-489-039A-7383
; Sequence 7383, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; FILE REFERENCE: 2709,2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 7383
; LENGTH: 374
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-7383

Query Match 72.9%; Score 35; DB 2; Length 374;
Best Local Similarity 85.7%; Pred. No. 74;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 DAPIGYD 8
Db 203 DAPAGYD 209

RESULT 30
US-09-252-991A-26250
; Sequence 26250, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196,136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 26250

LENGTH: 490
TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-26250

Query Match
Best Local Similarity 72.9%; Score 35; DB 2; Length 490;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 HDAPIGVD 8
DB 248 HDAPVGLD 255

RESULT 31
US-09-134-001C-3891
Sequence 3891, Application US/09134001C
Patent No. 6380370
GENERAL INFORMATION:
APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
FILE REFERENCE: GTC-007
CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR FILING DATE: 1997-11-08
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
SEQ ID NO 3891
LENGTH: 649
TYPE: PRT
ORGANISM: Staphylococcus epidermidis
US-09-134-001C-3891

Query Match
Best Local Similarity 72.9%; Score 35; DB 2; Length 649;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 HDAPIGVD 8
DB 339 HDLKIIGVD 346

RESULT 32
US-08-584-226-22
Sequence 22, Application US/08584226
Patent No. 5798240
GENERAL INFORMATION:
APPLICANT: Martinis, Susan A.
APPLICANT: Sasansfar, Mandana
APPLICANT: Kim, Sunghoon
APPLICANT: Lee, Sang Ho
APPLICANT: Schimmel, Paul R.
TITLE OF INVENTION: RECOMBINANT MYCOBACTERIAL METHIONYL-tRNA
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: Two Militia Drive
CITY: Lexington
STATE: Massachusetts
COUNTRY: USA
ZIP: 02173-4799
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/584,226
FILING DATE:

CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/305,766
FILING DATE: 13-SEP-1994
ATTORNEY/AGENT INFORMATION:
NAME: Brook, David E.
REGISTRATION NUMBER: 22,592
REFERENCE/DOCKET NUMBER: CP194-05Z
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-861-6240
TELEFAX: 617-861-9540
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-584-226-22

Query Match
Best Local Similarity 70.8%; Score 34; DB 1; Length 10;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DAPIGY 7
DB 5 DAPIGY 10

RESULT 33
US-09-747-287A-91
Sequence 91, Application US/09747287A
Patent No. 6893868
GENERAL INFORMATION:
APPLICANT: KOMORIYA, AKIRA
APPLICANT: PACKARD, BEVERLY S.
TITLE OF INVENTION: HOMO-DOUBLY LABELED COMPOSITIONS FOR THE DETECTION OF ENZYME
FILE REFERENCE: 300-948600US
CURRENT APPLICATION NUMBER: US/09/747,287A
CURRENT FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: US 09/349,019
PRIOR FILING DATE: 1999-09-10
PRIOR APPLICATION NUMBER: US08/802,981
PRIOR FILING DATE: 1997-02-20
PRIOR APPLICATION NUMBER: PCT/US00/24882
PRIOR FILING DATE: 2000-09-11
NUMBER OF SEQ ID NOS: 246
SOFTWARE: Patent version 3.3
SEQ ID NO 91
LENGTH: 16
TYPE: PRT
ORGANISM: Artificial
FEATURE:
OTHER INFORMATION: Synthetic peptide.
US-09-747-287A-91

Query Match
Best Local Similarity 70.8%; Score 34; DB 2; Length 16;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HDAPIG 6
DB 7 HDAPVG 12

RESULT 34
US-09-747-287A-92
Sequence 92, Application US/09747287A
Patent No. 6893868
GENERAL INFORMATION:
APPLICANT: KOMORIYA, AKIRA
APPLICANT: PACKARD, BEVERLY S.

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; TITLE OF INVENTION: HOMO-DOUBLY LABELED COMPOSITIONS FOR THE DETECTION OF ENZYME
; FILE REFERENCE: 300-948600US
; CURRENT FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US 09/747,287A
; PRIOR FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: US08/802,981
; PRIOR FILING DATE: 1997-02-20
; PRIOR APPLICATION NUMBER: PCT/US00/24882
; PRIOR FILING DATE: 2000-09-11
; NUMBER OF SEQ ID NOS: 246
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 92
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Synthetic peptide.
US-09-747-287A-92
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Query Match      70.8%; Score 34; DB 2; Length 16;
Best Local Similarity 83.3%; Pred. No. 4.2;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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```
OY      1 HDAPIG 6
        ||||:|
Db      7 HDAPVG 12
```

```
RESULT 35
US-09-747-287A-93
; Sequence 93, Application US/09747287A
; Patent No. 6893868
; GENERAL INFORMATION:
; APPLICANT: KOMORIYA, AKIRA
; TITLE OF INVENTION: HOMO-DOUBLY LABELED COMPOSITIONS FOR THE DETECTION OF ENZYME
; FILE REFERENCE: 300-948600US
; CURRENT APPLICATION NUMBER: US/09/747,287A
; CURRENT FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US 09/349,019
; PRIOR FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: US08/802,981
; PRIOR FILING DATE: 1997-02-20
; PRIOR APPLICATION NUMBER: PCT/US00/24882
; NUMBER OF SEQ ID NOS: 246
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 93
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Synthetic peptide.
US-09-747-287A-93
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```
Query Match      70.8%; Score 34; DB 2; Length 16;
Best Local Similarity 83.3%; Pred. No. 4.2;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
OY      1 HDAPIG 6
        ||||:|
Db      7 HDAPVG 12
```

```
RESULT 36
US-09-747-287A-206
; Sequence 206, Application US/09747287A
; Patent No. 6893868
; GENERAL INFORMATION:
; APPLICANT: KOMORIYA, AKIRA
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; APPLICANT: PACKARD, BEVERLY S.
; TITLE OF INVENTION: HOMO-DOUBLY LABELED COMPOSITIONS FOR THE DETECTION OF ENZYME
; FILE REFERENCE: 300-948600US
; CURRENT FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US 09/349,019
; PRIOR FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: US08/802,981
; PRIOR FILING DATE: 1997-02-20
; PRIOR APPLICATION NUMBER: PCT/US00/24882
; PRIOR FILING DATE: 2000-09-11
; NUMBER OF SEQ ID NOS: 246
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 206
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Synthetic peptide.
; NAME/KEY: misc feature
; LOCATION: (4)..(4)
; OTHER INFORMATION: Xaa is epsilon-aminocaproic acid
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (12)..(12)
; OTHER INFORMATION: Xaa is epsilon-aminocaproic acid
US-09-747-287A-206
```

```
Query Match      70.8%; Score 34; DB 2; Length 16;
Best Local Similarity 83.3%; Pred. No. 4.2;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
OY      1 HDAPIG 6
        ||||:|
Db      6 HDAPVG 11
```

```
RESULT 37
US-09-747-287A-94
; Sequence 94, Application US/09747287A
; Patent No. 6893868
; GENERAL INFORMATION:
; APPLICANT: KOMORIYA, AKIRA
; TITLE OF INVENTION: HOMO-DOUBLY LABELED COMPOSITIONS FOR THE DETECTION OF ENZYME
; FILE REFERENCE: 300-948600US
; CURRENT APPLICATION NUMBER: US/09/747,287A
; CURRENT FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US 09/349,019
; PRIOR FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: US08/802,981
; PRIOR FILING DATE: 1997-02-20
; PRIOR APPLICATION NUMBER: PCT/US00/24882
; PRIOR FILING DATE: 2000-09-11
; NUMBER OF SEQ ID NOS: 246
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 94
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Synthetic peptide.
; NAME/KEY: misc feature
; LOCATION: (4)..(4)
; OTHER INFORMATION: Xaa is epsilon-aminocaproic acid
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (14)..(14)
; OTHER INFORMATION: Xaa is epsilon-aminocaproic acid
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US-09-747-287A-94

Query Match 70.8%; Score 34; DB 2; Length 18;
Best Local Similarity 83.3%; Pred. No. 4.8;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HDAPIG 6
|||:|
Db 8 HDAPVG 13

RESULT 38

US-09-747-287A-95
Sequence 95, Application US/09747287A
Patent No. 6893868

GENERAL INFORMATION:

APPLICANT: KOMORIYA, AKIRA

APPLICANT: PACKARD, BEVERLY S.

TITLE OF INVENTION: HOMO-DOUBLY LABELED COMPOSITIONS FOR THE DETECTION OF ENZYME

FILE REFERENCE: 300-948600US

CURRENT FILING DATE: 2000-12-22

PRIOR APPLICATION NUMBER: US 09/349,019

PRIOR FILING DATE: 1999-09-10

PRIOR APPLICATION NUMBER: US08/802,981

PRIOR FILING DATE: 1997-02-20

PRIOR APPLICATION NUMBER: PCT/US00/24882

PRIOR FILING DATE: 2000-09-11

NUMBER OF SEQ ID NOS: 246

SOFTWARE: PatentIn version 3.3

SEQ ID NO 95

LENGTH: 18

TYPE: PRT

ORGANISM: Artificial

FEATURE:

OTHER INFORMATION: Synthetic peptide.

FEATURE:

NAME/KEY: misc_feature

LOCATION: (4)..(4)

OTHER INFORMATION: Xaa is epsilon-aminocaproic acid

FEATURE:

NAME/KEY: misc_feature

LOCATION: (14)..(14)

OTHER INFORMATION: Xaa is epsilon-aminocaproic acid

US-09-747-287A-95

Query Match 70.8%; Score 34; DB 2; Length 18;
Best Local Similarity 83.3%; Pred. No. 4.8;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HDAPIG 6
|||:|
Db 8 HDAPVG 13

RESULT 39

US-09-747-287A-96
Sequence 96, Application US/09747287A
Patent No. 6893868

GENERAL INFORMATION:

APPLICANT: KOMORIYA, AKIRA

APPLICANT: PACKARD, BEVERLY S.

TITLE OF INVENTION: HOMO-DOUBLY LABELED COMPOSITIONS FOR THE DETECTION OF ENZYME

FILE REFERENCE: 300-948600US

CURRENT FILING DATE: 2000-12-22

PRIOR APPLICATION NUMBER: US 09/349,019

PRIOR FILING DATE: 1999-09-10

PRIOR APPLICATION NUMBER: US08/802,981

PRIOR FILING DATE: 1997-02-20

PRIOR APPLICATION NUMBER: PCT/US00/24882

PRIOR FILING DATE: 2000-09-11
NUMBER OF SEQ ID NOS: 246
SOFTWARE: PatentIn version 3.3
SEQ ID NO 96

LENGTH: 18

TYPE: PRT

ORGANISM: Artificial

FEATURE:

OTHER INFORMATION: Synthetic peptide.

FEATURE:

NAME/KEY: misc_feature

LOCATION: (4)..(4)

OTHER INFORMATION: Xaa is epsilon-aminocaproic acid

FEATURE:

NAME/KEY: misc_feature

LOCATION: (14)..(14)

OTHER INFORMATION: Xaa is epsilon-aminocaproic acid

US-09-747-287A-96

Query Match 70.8%; Score 34; DB 2; Length 18;
Best Local Similarity 83.3%; Pred. No. 4.8;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HDAPIG 6
|||:|
Db 8 HDAPVG 13

RESULT 40

US-09-747-287A-97
Sequence 97, Application US/09747287A
Patent No. 6893868

GENERAL INFORMATION:

APPLICANT: KOMORIYA, AKIRA

APPLICANT: PACKARD, BEVERLY S.

TITLE OF INVENTION: HOMO-DOUBLY LABELED COMPOSITIONS FOR THE DETECTION OF ENZYME

FILE REFERENCE: 300-948600US

CURRENT FILING DATE: 2000-12-22

PRIOR APPLICATION NUMBER: US 09/349,019

PRIOR FILING DATE: 1999-09-10

PRIOR APPLICATION NUMBER: US08/802,981

PRIOR FILING DATE: 1997-02-20

PRIOR APPLICATION NUMBER: PCT/US00/24882

PRIOR FILING DATE: 2000-09-11

NUMBER OF SEQ ID NOS: 246

SOFTWARE: PatentIn version 3.3

SEQ ID NO 97

LENGTH: 18

TYPE: PRT

ORGANISM: Artificial

FEATURE:

OTHER INFORMATION: Synthetic peptide.

FEATURE:

NAME/KEY: misc_feature

LOCATION: (4)..(4)

OTHER INFORMATION: Xaa is epsilon-aminocaproic acid

FEATURE:

NAME/KEY: misc_feature

LOCATION: (14)..(14)

OTHER INFORMATION: Xaa is epsilon-aminocaproic acid

US-09-747-287A-97

Query Match 70.8%; Score 34; DB 2; Length 18;
Best Local Similarity 83.3%; Pred. No. 4.8;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HDAPIG 6
|||:|
Db 8 HDAPVG 13

Mon Dec 5 15:29:53 2005

us-10-807-553-2.ra1

Page 15

Search completed: December 3, 2005, 23:28:29
Job time : 25 secs

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OM protein - protein search, using sw model

Run on: December 3, 2005, 23:28:34 ; Search time 163 Seconds
(without alignments)
20.507 Million cell updates/sec

Title: US-10-807-553-2
Perfect score: 48
Sequence: 1 HDAPIGYD 8

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 41829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : Published Applications AA Main:
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2: /cgn2_6/ptodata/1/pubppaa/US08_PUBCOMB.pep:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	48	100.0	8	4	US-10-007-363-2
2	48	100.0	8	4	US-10-807-553-2
3	48	100.0	8	6	US-11-011-557-3
4	48	100.0	30	6	US-11-011-557-93
5	48	100.0	156	3	US-09-771-161A-104
6	48	100.0	737	3	US-09-771-161A-195
7	48	100.0	737	4	US-10-228-931-4
8	48	100.0	737	5	US-10-466-162-2
9	48	100.0	737	5	US-10-756-149-4713
10	44	91.7	8	4	US-10-007-363-7
11	44	91.7	8	4	US-10-007-363-13
12	44	91.7	8	4	US-10-807-553-7
13	44	91.7	8	4	US-10-807-553-13
14	44	91.7	8	6	US-11-011-557-9
15	44	91.7	8	6	US-11-011-557-15
16	44	91.7	8	6	US-11-011-557-31
17	44	89.6	8	4	US-10-007-363-8
18	43	89.6	8	4	US-10-807-553-8
19	43	89.6	8	6	US-11-011-557-10
20	43	89.6	8	6	US-11-011-557-55
21	42	87.5	8	4	US-10-007-363-9
22	42	87.5	8	4	US-10-807-553-9
23	42	87.5	8	6	US-11-011-557-11
24	42	87.5	8	6	US-11-011-557-29
25	40	83.3	8	4	US-10-007-363-12
26	40	83.3	8	4	US-10-007-363-14
27	40	83.3	8	4	US-10-807-553-12

28	40	83.3	8	4	US-10-807-553-14	Sequence 14, Appl
29	40	83.3	8	6	US-11-011-557-14	Sequence 14, Appl
30	40	83.3	8	6	US-11-011-557-16	Sequence 16, Appl
31	40	83.3	8	6	US-11-011-557-21	Sequence 21, Appl
32	40	83.3	8	6	US-11-011-557-79	Sequence 79, Appl
33	39	81.2	586	4	US-10-437-963-131067	Sequence 131067, Appl
34	39	81.2	719	4	US-10-437-963-172827	Sequence 172827, Appl
35	38	79.2	18	6	US-11-011-557-6	Sequence 6, Appl
36	38	79.2	35	4	US-10-199-820-290	Sequence 290, Appl
37	38	79.2	155	4	US-10-424-599-182799	Sequence 182799, Appl
38	38	79.2	682	5	US-10-466-162-4	Sequence 4, Appl
39	38	79.2	683	4	US-10-618-941-72	Sequence 72, Appl
40	38	79.2	683	5	US-10-973-858-40	Sequence 40, Appl
41	38	79.2	8	6	US-11-011-557-67	Sequence 67, Appl
42	37	77.1	171	4	US-10-437-963-123595	Sequence 123595, Appl
43	37	77.1	8	4	US-10-007-363-6	Sequence 6, Appl
44	36	75.0	8	4	US-10-007-363-17	Sequence 17, Appl
45	36	75.0	8	4	US-10-807-553-6	Sequence 6, Appl
46	36	75.0	8	4	US-10-807-553-17	Sequence 17, Appl
47	36	75.0	8	6	US-11-011-557-8	Sequence 8, Appl
48	36	75.0	8	6	US-11-011-557-19	Sequence 19, Appl
49	36	75.0	8	6	US-11-011-557-66	Sequence 66, Appl
50	36	75.0	54	4	US-10-425-115-256425	Sequence 256425, Appl
51	36	75.0	123	4	US-10-425-115-288608	Sequence 288608, Appl
52	36	75.0	396	4	US-10-424-599-276427	Sequence 276427, Appl
53	35	72.9	6	6	US-11-011-557-20	Sequence 20, Appl
54	35	72.9	8	4	US-10-007-363-10	Sequence 10, Appl
55	35	72.9	8	4	US-10-007-363-11	Sequence 11, Appl
56	35	72.9	8	4	US-10-807-553-11	Sequence 11, Appl
57	35	72.9	8	4	US-10-807-553-11	Sequence 11, Appl
58	35	72.9	8	6	US-11-011-557-12	Sequence 12, Appl
59	35	72.9	8	6	US-11-011-557-13	Sequence 13, Appl
60	35	72.9	8	6	US-11-011-557-32	Sequence 32, Appl
61	35	72.9	8	6	US-11-011-557-51	Sequence 51, Appl
62	35	72.9	8	6	US-11-011-557-53	Sequence 53, Appl
63	35	72.9	8	6	US-11-011-557-54	Sequence 54, Appl
64	35	72.9	8	6	US-11-011-557-56	Sequence 56, Appl
65	35	72.9	8	6	US-11-011-557-57	Sequence 57, Appl
66	35	72.9	14	3	US-09-747-287-207	Sequence 207, Appl
67	35	72.9	14	3	US-10-437-963-158408	Sequence 158408, Appl
68	35	72.9	74	4	US-10-425-115-320832	Sequence 320832, Appl
69	35	72.9	154	4	US-10-424-599-241213	Sequence 241213, Appl
70	35	72.9	192	4	US-10-767-701-51923	Sequence 51923, Appl
71	35	72.9	226	4	US-10-282-122A-71421	Sequence 71421, Appl
72	35	72.9	260	4	US-10-156-761-9832	Sequence 9832, Appl
73	35	72.9	287	3	US-09-925-301-1386	Sequence 1386, Appl
74	35	72.9	419	5	US-10-872-198-39	Sequence 39, Appl
75	35	72.9	419	5	US-10-872-197A-39	Sequence 39, Appl
76	35	72.9	419	6	US-11-021-951-39	Sequence 39, Appl
77	35	72.9	449	5	US-10-732-923-9276	Sequence 9276, Appl
78	35	72.9	455	4	US-10-437-963-171839	Sequence 171839, Appl
79	35	72.9	456	5	US-10-732-923-8916	Sequence 8916, Appl
80	35	72.9	456	5	US-10-631-467-1616	Sequence 1616, Appl
81	35	72.9	457	5	US-10-732-923-9090	Sequence 9090, Appl
82	35	72.9	457	5	US-10-732-923-9116	Sequence 9116, Appl
83	35	72.9	457	5	US-10-732-923-9267	Sequence 9267, Appl
84	35	72.9	457	5	US-10-732-923-9268	Sequence 9268, Appl
85	35	72.9	457	5	US-10-732-923-9275	Sequence 9275, Appl
86	35	72.9	457	5	US-10-732-923-9277	Sequence 9277, Appl
87	35	72.9	457	5	US-10-631-467-916	Sequence 916, Appl
88	35	72.9	457	5	US-10-369-493-178472	Sequence 178472, Appl
89	35	72.9	540	4	US-10-437-963-171847	Sequence 171847, Appl
90	35	72.9	644	4	US-10-282-122A-70835	Sequence 70835, Appl
91	35	72.9	644	4	US-10-724-972A-6325	Sequence 6325, Appl
92	35	72.9	793	5	US-10-450-763-55956	Sequence 55956, Appl
93	35	72.9	1247	5	US-10-450-763-55345	Sequence 55345, Appl
94	35	72.9	16	3	US-09-747-287-91	Sequence 91, Appl
95	34	70.8	16	3	US-09-747-287-92	Sequence 92, Appl
96	34	70.8	16	3	US-09-747-287-93	Sequence 93, Appl
97	34	70.8	16	3	US-09-747-287-206	Sequence 206, Appl
98	34	70.8	16	3	US-09-874-350A-58	Sequence 58, Appl
99	34	70.8	16	3	US-09-874-350A-59	Sequence 59, Appl
100	34	70.8	16	3	US-09-874-350A-59	Sequence 59, Appl

ALIGNMENTS

ABM

RESULT 1
US-10-007-363-2
Sequence 2, Application US/10007363
Publication No. US20020168354A1
GENERAL INFORMATION:
APPLICANT: Mochly-Rosen, Daria
TITLE OF INVENTION: pseudo-epsilon RACK Peptide Composition
TITLE OF INVENTION: and Method for Protection Against Tissue Damage Due to
TITLE OF INVENTION: Ischemia
FILE REFERENCE: 58600-8209-US00
CURRENT APPLICATION NUMBER: US/10/007,363
CURRENT FILING DATE: 2002-11-09
PRIOR APPLICATION NUMBER: US 60/247,830
PRIOR FILING DATE: 2000-11-10
NUMBER OF SEQ ID NOS: 18
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 2
LENGTH: 8
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: pseudo-epsilon RACK octapeptide
US-10-007-363-2

Query Match
Best Local Similarity 100.0%; Score 48; DB 4; Length 8;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HDAPIGYD 8
Db 1 HDAPIGYD 8

mine

RESULT 2
US-10-807-553-2
Sequence 2, Application US/10807553
Publication No. US2004018655A1
GENERAL INFORMATION:
APPLICANT: Mochly-Rosen, Daria
TITLE OF INVENTION: pseudo-epsilon RACK Peptide Composition
TITLE OF INVENTION: and Method for Protection Against Tissue Damage Due to
TITLE OF INVENTION: Ischemia
FILE REFERENCE: 58600-8209-US00
CURRENT APPLICATION NUMBER: US/10/807,553
CURRENT FILING DATE: 2004-03-22
PRIOR APPLICATION NUMBER: US/10/007,363
PRIOR FILING DATE: 2001-11-09
PRIOR APPLICATION NUMBER: US 60/247,830
PRIOR FILING DATE: 2000-11-10
NUMBER OF SEQ ID NOS: 18
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 2
LENGTH: 8
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: pseudo-epsilon RACK octapeptide
US-10-807-553-2

Query Match
Best Local Similarity 100.0%; Score 48; DB 4; Length 8;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HDAPIGYD 8
Db 1 HDAPIGYD 8

RESULT 3
US-11-011-557-3
Sequence 3, Application US/11011557
Publication No. US20050187156A1
GENERAL INFORMATION:
APPLICANT: Mochly-Rosen, Daria
TITLE OF INVENTION: Isozyme-Specific Antagonists of Protein Kinase C
FILE REFERENCE: 58600-8212-US00
CURRENT APPLICATION NUMBER: US/11/011,557
CURRENT FILING DATE: 2004-12-13
PRIOR APPLICATION NUMBER: 60/529,223
PRIOR FILING DATE: 2003-12-11
NUMBER OF SEQ ID NOS: 97
SOFTWARE: PatentIn version 3.3
SEQ ID NO 3
LENGTH: 8
TYPE: PRT
ORGANISM: Homo sapiens
US-11-011-557-3

no chr's
to inv.

Query Match
Best Local Similarity 100.0%; Score 48; DB 6; Length 8;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HDAPIGYD 8
Db 1 HDAPIGYD 8

RESULT 4
US-11-011-557-93
Sequence 93, Application US/11011557
Publication No. US20050187156A1
GENERAL INFORMATION:
APPLICANT: Mochly-Rosen, Daria
TITLE OF INVENTION: Isozyme-Specific Antagonists of Protein Kinase C
FILE REFERENCE: 58600-8212-US00
CURRENT APPLICATION NUMBER: US/11/011,557
CURRENT FILING DATE: 2004-12-13
PRIOR APPLICATION NUMBER: 60/529,223
PRIOR FILING DATE: 2003-12-11
NUMBER OF SEQ ID NOS: 97
SOFTWARE: PatentIn version 3.3
SEQ ID NO 93
LENGTH: 30
TYPE: PRT
ORGANISM: Homo sapiens
US-11-011-557-93

Query Match
Best Local Similarity 100.0%; Score 48; DB 6; Length 30;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HDAPIGYD 8
Db 15 HDAPIGYD 22

RESULT 5
US-09-771-161A-104
Sequence 104, Application US/09771161A
Patent No. US20020110811A1
GENERAL INFORMATION:
APPLICANT: LEVINE, et al.
TITLE OF INVENTION: VARIANTS OF PROTEIN KINASES
FILE REFERENCE: 802620-2005.1
CURRENT APPLICATION NUMBER: US/09/771,161A
CURRENT FILING DATE: 2001-01-26
PRIOR APPLICATION NUMBER: 09/724,636
PRIOR FILING DATE: 2000-11-28
PRIOR APPLICATION NUMBER: 09/724,636

PRIOR FILING DATE: 2000-06-15
PRIOR APPLICATION NUMBER: 135619
PRIOR FILING DATE: 2000-04-12
NUMBER OF SEQ ID NOS: 273
SOFTWARE: PatentIn version 3.0
SEQ ID NO 104
LENGTH: 156
TYPE: PRT
ORGANISM: Homo sapiens
US-09-771-161A-104

Query Match 100.0%; Score 48; DB 3; Length 156;
Best Local Similarity 100.0%; Pred. No. 0.28;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 HDAPIGYD 8
DB 85 HDAPIGYD 92

RESULT 6
US-09-771-161A-195
Sequence 195, Application US/09771161A
Patent No. US20020110811A1
GENERAL INFORMATION:
APPLICANT: LEVINE, et al.
TITLE OF INVENTION: VARIANTS OF PROTEIN KINASES
FILE REFERENCE: 802620-2005.1
CURRENT APPLICATION NUMBER: US/09/771,161A
CURRENT FILING DATE: 2001-01-26
PRIOR APPLICATION NUMBER: 09/724,676
PRIOR FILING DATE: 2000-11-28
PRIOR APPLICATION NUMBER: 136776
PRIOR FILING DATE: 2000-06-15
PRIOR APPLICATION NUMBER: 135619
PRIOR FILING DATE: 2000-04-12
NUMBER OF SEQ ID NOS: 273
SOFTWARE: PatentIn version 3.0
SEQ ID NO 195
LENGTH: 737
TYPE: PRT
ORGANISM: Homo sapiens
US-09-771-161A-195

Query Match 100.0%; Score 48; DB 3; Length 737;
Best Local Similarity 100.0%; Pred. No. 1.4;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 HDAPIGYD 8
DB 85 HDAPIGYD 92

RESULT 7
US-10-228-931-4
Sequence 4, Application US/10228931
Publication No. US20030051258A1
GENERAL INFORMATION:
APPLICANT: Verma, Ajit K
APPLICANT: Reddig, Peter J
APPLICANT: Jansen, Aaron P
TITLE OF INVENTION: Animal Model System for Squamous Cell Carcinoma
FILE REFERENCE: 960236.97613
CURRENT APPLICATION NUMBER: US/10/228,931
CURRENT FILING DATE: 2002-08-27
PRIOR APPLICATION NUMBER: US/09/772,647
PRIOR FILING DATE: 2001-01-30
NUMBER OF SEQ ID NOS: 6
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 4
LENGTH: 737
TYPE: PRT
ORGANISM: Artificial Sequence

FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: T7 tag and
OTHER INFORMATION: mouse protein kinase C epsilon coding sequence
US-10-228-931-4

Query Match 100.0%; Score 48; DB 4; Length 737;
Best Local Similarity 100.0%; Pred. No. 1.4;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 HDAPIGYD 8
DB 85 HDAPIGYD 92

RESULT 8
US-10-466-162-2
Sequence 2, Application US/10466162
Publication No. US20050170343A1
GENERAL INFORMATION:
APPLICANT: EXELIXIS, INC.
TITLE OF INVENTION: Modulating Insulin Receptor Signaling
FILE REFERENCE: EX02-001C-PC
CURRENT APPLICATION NUMBER: US/10/466,162
CURRENT FILING DATE: 2003-07-11
PRIOR APPLICATION NUMBER: US 60/261,335
PRIOR FILING DATE: 2001-01-12
PRIOR APPLICATION NUMBER: US 60/261,694
PRIOR FILING DATE: 2001-01-12
PRIOR APPLICATION NUMBER: US 60/261,532
PRIOR FILING DATE: 2001-01-12
PRIOR APPLICATION NUMBER: US 60/261,361
PRIOR FILING DATE: 2001-01-12
PRIOR APPLICATION NUMBER: US 60/261,531
PRIOR FILING DATE: 2001-01-12
PRIOR APPLICATION NUMBER: US 60/261,457
PRIOR FILING DATE: 2001-01-12
PRIOR APPLICATION NUMBER: US 60/261,226
PRIOR FILING DATE: 2001-01-12
PRIOR APPLICATION NUMBER: US 60/261,304
PRIOR FILING DATE: 2001-01-12
PRIOR APPLICATION NUMBER: US 60/261,459
PRIOR FILING DATE: 2001-01-12
PRIOR APPLICATION NUMBER: US 60/261,456
PRIOR FILING DATE: 2001-01-12
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 76
SOFTWARE: PatentIn version 3.1
SEQ ID NO 2
LENGTH: 737
TYPE: PRT
ORGANISM: Homo sapiens
US-10-466-162-2

Query Match 100.0%; Score 48; DB 5; Length 737;
Best Local Similarity 100.0%; Pred. No. 1.4;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 HDAPIGYD 8
DB 85 HDAPIGYD 92

RESULT 9
US-10-756-149-4713
Sequence 4713, Application US/10756149
Publication No. US20050181375A1
GENERAL INFORMATION:
APPLICANT: Azizi, Natasha
APPLICANT: Zlotnik, Albert
TITLE OF INVENTION: NOVEL METHODS OF DIAGNOSIS OF METASTATIC CANCER, COMPOSITIONS AND
METHODS OF SCREENING FOR MODULATORS OF METASTATIC CANCER
FILE REFERENCE: file
CURRENT APPLICATION NUMBER: US/10/756,149

CURRENT FILING DATE: 2004-01-12
NUMBER OF SEQ ID NOS: 5818
SOFTWARE: PatentIn version 3.2
SEQ ID NO 4713
LENGTH: 737
TYPE: PRT
ORGANISM: Homo Sapiens
US-10-756-149-4713

Query Match 100.0%; Score 48; DB 5; Length 737;
Best Local Similarity 100.0%; Pred. No. 1.4;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HDAPIGYD 8
Db 85 HDAPIGYD 92

RESULT 10
US-10-007-363-7
Sequence 7, Application US/10007363
Publication No. US20020168354A1
GENERAL INFORMATION:

ABN

APPLICANT: Mochly-Rosen, Daria
TITLE OF INVENTION: pseudo-epsilon RACK Peptide Composition
TITLE OF INVENTION: and Method for Protection Against Tissue Damage Due to
FILE REFERENCE: 58600-8209.US00
CURRENT APPLICATION NUMBER: US/10/007,363
CURRENT FILING DATE: 2002-11-09
PRIOR APPLICATION NUMBER: US 60/247,830
PRIOR FILING DATE: 2000-11-10
NUMBER OF SEQ ID NOS: 18
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 7
LENGTH: 8
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: modified pseudo-epsilon RACK peptide
US-10-007-363-7

Query Match 91.7%; Score 44; DB 4; Length 8;
Best Local Similarity 87.5%; Pred. No. 1.7e+06;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HDAPIGYD 8
Db 1 HDAPIGYD 8

RESULT 11
US-10-007-363-13
Sequence 13, Application US/10007363
Publication No. US20020168354A1
GENERAL INFORMATION:

APPLICANT: Mochly-Rosen, Daria
TITLE OF INVENTION: pseudo-epsilon RACK Peptide Composition
TITLE OF INVENTION: and Method for Protection Against Tissue Damage Due to
FILE REFERENCE: 58600-8209.US00
CURRENT APPLICATION NUMBER: US/10/007,363
CURRENT FILING DATE: 2002-11-09
PRIOR APPLICATION NUMBER: US 60/247,830
PRIOR FILING DATE: 2000-11-10
NUMBER OF SEQ ID NOS: 18
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 13
LENGTH: 8
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: modified pseudo-epsilon RACK peptide

US-10-007-363-13

Query Match 91.7%; Score 44; DB 4; Length 8;
Best Local Similarity 87.5%; Pred. No. 1.7e+06;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 HDAPIGYD 8
Db 1 HDAPIGYD 8

RESULT 12
US-10-807-553-7
Sequence 7, Application US/10807553
Publication No. US20040186055A1
GENERAL INFORMATION:

APPLICANT: Mochly-Rosen, Daria
TITLE OF INVENTION: pseudo-epsilon RACK Peptide Composition
TITLE OF INVENTION: and Method for Protection Against Tissue Damage Due to
FILE REFERENCE: 58600-8209.US00
CURRENT APPLICATION NUMBER: US/10/807,553
CURRENT FILING DATE: 2004-03-22
PRIOR APPLICATION NUMBER: US/10/007,363
PRIOR FILING DATE: 2001-11-09
PRIOR APPLICATION NUMBER: US 60/247,830
PRIOR FILING DATE: 2000-11-10
NUMBER OF SEQ ID NOS: 18
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 7
LENGTH: 8
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: modified pseudo-epsilon RACK peptide
US-10-807-553-7

Query Match 91.7%; Score 44; DB 4; Length 8;
Best Local Similarity 87.5%; Pred. No. 1.7e+06;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HDAPIGYD 8
Db 1 HDAPIGYD 8

RESULT 13
US-10-807-553-13
Sequence 13, Application US/10807553
Publication No. US20040186055A1
GENERAL INFORMATION:

APPLICANT: Mochly-Rosen, Daria
TITLE OF INVENTION: pseudo-epsilon RACK Peptide Composition
TITLE OF INVENTION: and Method for Protection Against Tissue Damage Due to
FILE REFERENCE: 58600-8209.US00
CURRENT APPLICATION NUMBER: US/10/807,553
CURRENT FILING DATE: 2004-03-22
PRIOR APPLICATION NUMBER: US/10/007,363
PRIOR FILING DATE: 2001-11-09
PRIOR APPLICATION NUMBER: US 60/247,830
PRIOR FILING DATE: 2000-11-10
NUMBER OF SEQ ID NOS: 18
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 13
LENGTH: 8
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: modified pseudo-epsilon RACK peptide
US-10-807-553-13

Query Match 91.7%; Score 44; DB 4; Length 8;

QY 1 HDAPIGYD 8

Best Local Similarity 87.5%; Pred. No. 1.7e+06;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 HDAPIGVD 8
Db 1 HDGPIGVD 8

NO C/S INU

RESULT 14
US-11-011-557-9
Sequence 9, Application US/11011557
Publication No. US20050187156A1
GENERAL INFORMATION:
APPLICANT: Mochly-Rosen, Daria
TITLE OF INVENTION: Isozyme-Specific Antagonists of Protein Kinase C
FILE REFERENCE: 58600-8212.US00
CURRENT APPLICATION NUMBER: US/11/011,557
CURRENT FILING DATE: 2004-12-13
PRIOR APPLICATION NUMBER: 60/529,223
PRIOR FILING DATE: 2003-12-11
NUMBER OF SEQ ID NOS: 97
SOFTWARE: PatentIn version 3.3
SEQ ID NO 9
LENGTH: 8
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Alternative pseudo-epsilon RACK peptide
US-11-011-557-9

Query Match 91.7%; Score 44; DB 6; Length 8;
Best Local Similarity 87.5%; Pred. No. 1.7e+06;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HDAPIGVD 8
Db 1 HDAPIGVE 8

RESULT 15
US-11-011-557-15
Sequence 15, Application US/11011557
Publication No. US20050187156A1
GENERAL INFORMATION:
APPLICANT: Mochly-Rosen, Daria
TITLE OF INVENTION: Isozyme-Specific Antagonists of Protein Kinase C
FILE REFERENCE: 58600-8212.US00
CURRENT APPLICATION NUMBER: US/11/011,557
CURRENT FILING DATE: 2004-12-13
PRIOR APPLICATION NUMBER: 60/529,223
PRIOR FILING DATE: 2003-12-11
NUMBER OF SEQ ID NOS: 97
SOFTWARE: PatentIn version 3.3
SEQ ID NO 15
LENGTH: 8
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Alternative pseudo-epsilon RACK peptide
US-11-011-557-15

Query Match 91.7%; Score 44; DB 6; Length 8;
Best Local Similarity 87.5%; Pred. No. 1.7e+06;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 HDAPIGVD 8
Db 1 HDGPIGVD 8

RESULT 16

US-11-011-557-31
Sequence 31, Application US/11011557
Publication No. US20050187156A1
GENERAL INFORMATION:
APPLICANT: Mochly-Rosen, Daria
TITLE OF INVENTION: Isozyme-Specific Antagonists of Protein Kinase C
FILE REFERENCE: 58600-8212.US00
CURRENT APPLICATION NUMBER: US/11/011,557
CURRENT FILING DATE: 2004-12-13
PRIOR APPLICATION NUMBER: 60/529,223
PRIOR FILING DATE: 2003-12-11
NUMBER OF SEQ ID NOS: 97
SOFTWARE: PatentIn version 3.3
SEQ ID NO 31
LENGTH: 8
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Alternative pseudo-eta RACK peptide
US-11-011-557-31

Query Match 91.7%; Score 44; DB 6; Length 8;
Best Local Similarity 87.5%; Pred. No. 1.7e+06;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 HDAPIGVD 8
Db 1 HDTPIGVD 8

RESULT 17
US-10-007-363-8
Sequence 8, Application US/10007363
Publication No. US20020168354A1
GENERAL INFORMATION:
APPLICANT: Mochly-Rosen, Daria
TITLE OF INVENTION: pseudo-epsilon RACK Peptide Composition
TITLE OF INVENTION: and Method for Protection Against Tissue Damage Due to
FILE REFERENCE: 58600-8209.US00
CURRENT APPLICATION NUMBER: US/10/007,363
CURRENT FILING DATE: 2002-11-09
PRIOR APPLICATION NUMBER: US 60/247,830
PRIOR FILING DATE: 2000-11-10
NUMBER OF SEQ ID NOS: 18
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 8
LENGTH: 8
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: modified pseudo-epsilon RACK peptide
US-10-007-363-8

Query Match 89.6%; Score 43; DB 4; Length 8;
Best Local Similarity 75.0%; Pred. No. 1.7e+06;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HDAPIGVD 8
Db 1 HDAPVIGVE 8

RESULT 18
US-10-807-553-8
Sequence 8, Application US/10807553
Publication No. US20040186055A1
GENERAL INFORMATION:
APPLICANT: Mochly-Rosen, Daria
TITLE OF INVENTION: pseudo-epsilon RACK Peptide Composition
TITLE OF INVENTION: and Method for Protection Against Tissue Damage Due to
Ischemia

```
FILE REFERENCE: 58600-8209.US00
CURRENT APPLICATION NUMBER: US/10/807,553
CURRENT FILING DATE: 2004-03-22
PRIOR APPLICATION NUMBER: US/10/007,363
PRIOR FILING DATE: 2001-11-09
PRIOR APPLICATION NUMBER: US 60/247,830
PRIOR FILING DATE: 2000-11-10
NUMBER OF SEQ ID NOS: 18
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 8
LENGTH: 8
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: modified pseudo-epsilon RACK peptide
US-10-807-553-8
```

```
Query Match      89.6%; Score 43; DB 4; Length 8;
Best Local Similarity 75.0%; Pred. No. 1.7e+06;
Matches 6; Conservative 2; Mismatches 0; Gaps 0;
```

```
Oy      1 HDAPIGYD 8
        |||||:
Db      1 HDAPVGYR 8
```

```
RESULT 19
US-11-011-557-10
Sequence 10, Application US/11011557
Publication No. US20050187156A1
GENERAL INFORMATION:
APPLICANT: Mochly-Rosen, Daria
TITLE OF INVENTION: Isozyme-Specific Antagonists of Protein Kinase C
FILE REFERENCE: 58600-8212.US00
CURRENT FILING DATE: 2004-12-13
PRIOR APPLICATION NUMBER: 60/529,223
PRIOR FILING DATE: 2003-12-11
NUMBER OF SEQ ID NOS: 97
SOFTWARE: PatentIn version 3.3
SEQ ID NO 10
LENGTH: 8
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Alternative pseudo-epsilon RACK peptide
US-11-011-557-10
```

```
Query Match      89.6%; Score 43; DB 6; Length 8;
Best Local Similarity 75.0%; Pred. No. 1.7e+06;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
```

```
Oy      1 HDAPIGYD 8
        |||||:
Db      1 HDAPVGYR 8
```

```
RESULT 20
US-11-011-557-55
Sequence 55, Application US/11011557
Publication No. US20050187156A1
GENERAL INFORMATION:
APPLICANT: Chen, Leon E.
TITLE OF INVENTION: Isozyme-Specific Antagonists of Protein Kinase C
FILE REFERENCE: 58600-8212.US00
CURRENT FILING DATE: 2004-12-13
PRIOR APPLICATION NUMBER: 60/529,223
PRIOR FILING DATE: 2003-12-11
NUMBER OF SEQ ID NOS: 97
SOFTWARE: PatentIn version 3.3
```

```
SEQ ID NO 55
LENGTH: 8
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: A modification of SEQ ID NO:3
US-11-011-557-55
```

```
Query Match      89.6%; Score 43; DB 6; Length 8;
Best Local Similarity 87.5%; Pred. No. 1.7e+06;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
Oy      1 HDAPIGYD 8
        |||||:
Db      1 HNAPIGYD 8
```

```
RESULT 21
US-10-007-363-9
Sequence 9, Application US/10007363
Publication No. US20020168354A1
GENERAL INFORMATION:
APPLICANT: Mochly-Rosen, Daria
TITLE OF INVENTION: pseudo-epsilon RACK Peptide Composition
and Method for Protection Against Tissue Damage Due to
TITLE OF INVENTION: Ischemia
FILE REFERENCE: 58600-8209.US00
CURRENT FILING DATE: 2002-11-09
PRIOR APPLICATION NUMBER: US 60/247,830
PRIOR FILING DATE: 2000-11-10
NUMBER OF SEQ ID NOS: 18
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 9
LENGTH: 8
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: modified pseudo-epsilon RACK peptide
US-10-007-363-9
```

```
Query Match      87.5%; Score 42; DB 4; Length 8;
Best Local Similarity 75.0%; Pred. No. 1.7e+06;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
```

```
Oy      1 HDAPIGYD 8
        |||||:
Db      1 HDAPVGYR 8
```

```
RESULT 22
US-10-807-553-9
Sequence 9, Application US/10807553
Publication No. US20040186055A1
GENERAL INFORMATION:
APPLICANT: Mochly-Rosen, Daria
TITLE OF INVENTION: pseudo-epsilon RACK Peptide Composition
and Method for Protection Against Tissue Damage Due to
TITLE OF INVENTION: Ischemia
FILE REFERENCE: 58600-8209.US00
CURRENT FILING DATE: 2004-03-22
PRIOR APPLICATION NUMBER: US/10/007,363
PRIOR FILING DATE: 2001-11-09
PRIOR APPLICATION NUMBER: US 60/247,830
PRIOR FILING DATE: 2000-11-10
NUMBER OF SEQ ID NOS: 18
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 9
LENGTH: 8
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
```

OTHER INFORMATION: modified pseudo-epsilon RACK peptide
US-10-807-553-9

Query Match 87.5%; Score 42; DB 4; Length 8;
Best Local Similarity 75.0%; Pred. No. 1.7e+06;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 HDAPIGYD 8
Db 1 HDAPLGYE 8

RESULT 23

US-11-011-557-11
Sequence 11, Application US/11011557
Publication No. US20050187156A1
GENERAL INFORMATION:
APPLICANT: Mochly-Rosen, Daria
APPLICANT: Chen, Leon E.
TITLE OF INVENTION: Isozyme-Specific Antagonists of Protein Kinase C
FILE REFERENCE: 58600-8212.US00
CURRENT FILING DATE: 2004-12-13
PRIOR APPLICATION NUMBER: US/11/011,557
PRIOR FILING DATE: 2003-12-11
NUMBER OF SEQ ID NOS: 97
SOFTWARE: Patentin version 3.3
SEQ ID NO 11
LENGTH: 8
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Alternative pseudo-epsilon RACK peptide
US-11-011-557-11

Query Match 87.5%; Score 42; DB 6; Length 8;
Best Local Similarity 75.0%; Pred. No. 1.7e+06;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 HDAPIGYD 8
Db 1 HDAPLGYE 8

RESULT 24

US-11-011-557-29
Sequence 29, Application US/11011557
Publication No. US20050187156A1
GENERAL INFORMATION:
APPLICANT: Mochly-Rosen, Daria
APPLICANT: Chen, Leon E.
TITLE OF INVENTION: Isozyme-Specific Antagonists of Protein Kinase C
FILE REFERENCE: 58600-8212.US00
CURRENT FILING DATE: 2004-12-13
PRIOR APPLICATION NUMBER: US/11/011,557
PRIOR FILING DATE: 2003-12-11
NUMBER OF SEQ ID NOS: 97
SOFTWARE: Patentin version 3.3
SEQ ID NO 29
LENGTH: 8
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Alternative pseudo-eta RACK peptide
US-11-011-557-29

Query Match 87.5%; Score 42; DB 6; Length 8;
Best Local Similarity 75.0%; Pred. No. 1.7e+06;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 HDAPIGYD 8
Db 1 HDAPLGYE 8

Db 1 HDPELGYD 8

RESULT 25
US-10-007-363-12
Sequence 12, Application US/10007363
Publication No. US20020168354A1
GENERAL INFORMATION:
APPLICANT: Mochly-Rosen, Daria
TITLE OF INVENTION: pseudo-epsilon RACK Peptide Composition
TITLE OF INVENTION: and Method for Protection Against Tissue Damage Due to
FILE REFERENCE: 58600-8209.US00
CURRENT FILING DATE: 2002-11-09
PRIOR APPLICATION NUMBER: US/10/007,363
PRIOR FILING DATE: 2000-11-10
NUMBER OF SEQ ID NOS: 18
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 12
LENGTH: 8
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: modified pseudo-epsilon RACK peptide
US-10-007-363-12

Query Match 83.3%; Score 40; DB 4; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DAPIGYD 8
Db 2 DAPIGYD 8

RESULT 26

US-10-007-363-14
Sequence 14, Application US/10007363
Publication No. US20020168354A1
GENERAL INFORMATION:
APPLICANT: Mochly-Rosen, Daria
TITLE OF INVENTION: pseudo-epsilon RACK Peptide Composition
TITLE OF INVENTION: and Method for Protection Against Tissue Damage Due to
FILE REFERENCE: 58600-8209.US00
CURRENT FILING DATE: 2002-11-09
PRIOR APPLICATION NUMBER: US/10/007,363
PRIOR FILING DATE: 2000-11-10
NUMBER OF SEQ ID NOS: 18
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 14
LENGTH: 8
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: modified pseudo-epsilon RACK peptide
US-10-007-363-14

Query Match 83.3%; Score 40; DB 4; Length 8;
Best Local Similarity 87.5%; Pred. No. 1.7e+06;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 HDAPIGYD 8
Db 1 HDAPLGYD 8

RESULT 27
US-10-807-553-12
Sequence 12, Application US/10807553
Publication No. US20040186055A1

```
; GENERAL INFORMATION:
; APPLICANT: Mochly-Rosen, Daria
; TITLE OF INVENTION: pseudo-epsilon RACK Peptide Composition
; TITLE OF INVENTION: and Method for Protection Against Tissue Damage Due to
; TITLE OF INVENTION: Ischemia
; FILE REFERENCE: 58600-8209.US00
; CURRENT APPLICATION NUMBER: US/10/807,553
; CURRENT FILING DATE: 2004-03-22
; PRIOR APPLICATION NUMBER: US/10/007,363
; PRIOR FILING DATE: 2001-11-09
; PRIOR APPLICATION NUMBER: US 60/247,830
; PRIOR FILING DATE: 2000-11-10
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: modified pseudo-epsilon RACK peptide
US-10-807-553-12
```

```
Query Match      83.3%; Score 40; DB 4; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      2 DAPIGYD 8
        |||||
Db       2 DAPIGYD 8
```

```
RESULT 28
US-10-807-553-14
; Sequence 14, Application US/10807553
; Publication No. US20040186655A1
; GENERAL INFORMATION:
; APPLICANT: Mochly-Rosen, Daria
; TITLE OF INVENTION: pseudo-epsilon RACK Peptide Composition
; TITLE OF INVENTION: and Method for Protection Against Tissue Damage Due to
; TITLE OF INVENTION: Ischemia
; FILE REFERENCE: 58600-8209.US00
; CURRENT APPLICATION NUMBER: US/10/807,553
; CURRENT FILING DATE: 2004-03-22
; PRIOR APPLICATION NUMBER: US/10/007,363
; PRIOR FILING DATE: 2001-11-09
; PRIOR APPLICATION NUMBER: US 60/247,830
; PRIOR FILING DATE: 2000-11-10
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: modified pseudo-epsilon RACK peptide
US-10-807-553-14
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Query Match      83.3%; Score 40; DB 4; Length 8;
Best Local Similarity 87.5%; Pred. No. 1.7e+06;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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QY      1 HDAPIGYD 8
        |||||
Db       1 HDAPIGYD 8
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RESULT 29
US-11-011-557-14
; Sequence 14, Application US/11011557
; Publication No. US20050187156A1
; GENERAL INFORMATION:
; APPLICANT: Mochly-Rosen, Daria
; APPLICANT: Chen, Leon E.
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```
; TITLE OF INVENTION: Isozyme-Specific Antagonists of Protein Kinase C
; FILE REFERENCE: 58600-8212.US00
; CURRENT APPLICATION NUMBER: US/11/011,557
; CURRENT FILING DATE: 2004-12-13
; PRIOR APPLICATION NUMBER: 60/529,223
; PRIOR FILING DATE: 2003-12-11
; NUMBER OF SEQ ID NOS: 97
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 14
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Alternative pseudo-epsilon RACK peptide
US-11-011-557-14
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Query Match      83.3%; Score 40; DB 6; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY      2 DAPIGYD 8
        |||||
Db       2 DAPIGYD 8
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RESULT 30
US-11-011-557-16
; Sequence 16, Application US/11011557
; Publication No. US20050187156A1
; GENERAL INFORMATION:
; APPLICANT: Mochly-Rosen, Daria
; APPLICANT: Chen, Leon E.
; TITLE OF INVENTION: Isozyme-Specific Antagonists of Protein Kinase C
; FILE REFERENCE: 58600-8212.US00
; CURRENT APPLICATION NUMBER: US/11/011,557
; CURRENT FILING DATE: 2004-12-13
; PRIOR APPLICATION NUMBER: 60/529,223
; PRIOR FILING DATE: 2003-12-11
; NUMBER OF SEQ ID NOS: 97
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 16
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Alternative pseudo-epsilon RACK peptide
US-11-011-557-16
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Query Match      83.3%; Score 40; DB 6; Length 8;
Best Local Similarity 87.5%; Pred. No. 1.7e+06;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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```
QY      1 HDAPIGYD 8
        |||||
Db       1 HDAPIGYD 8
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RESULT 31
US-11-011-557-21
; Sequence 21, Application US/11011557
; Publication No. US20050187156A1
; GENERAL INFORMATION:
; APPLICANT: Mochly-Rosen, Daria
; APPLICANT: Chen, Leon E.
; TITLE OF INVENTION: Isozyme-Specific Antagonists of Protein Kinase C
; FILE REFERENCE: 58600-8212.US00
; CURRENT APPLICATION NUMBER: US/11/011,557
; CURRENT FILING DATE: 2004-12-13
; PRIOR APPLICATION NUMBER: 60/529,223
; PRIOR FILING DATE: 2003-12-11
; NUMBER OF SEQ ID NOS: 97
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 21
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; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Alternative pseudo-epsilon RACK peptide
US-11-011-557-21

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Query Match      83.3%; Score 40; DB 6; Length 8;
Best Local Similarity 87.5%; Pred. No. 1.7e+06;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY      1 HDAPIGYD 8
        |||||
Db      1 HDAPIDPYD 8

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RESULT 32
US-11-011-557-79
; Sequence 79, Application US/11011557
; Publication No. US20050187156A1
; GENERAL INFORMATION:
; APPLICANT: Mochly-Rosen, Daria
; APPLICANT: Chen, Leon E.
; TITLE OF INVENTION: Isozyme-Specific Antagonists of Protein Kinase C
; FILE REFERENCE: 58600-8212.US00
; CURRENT APPLICATION NUMBER: US/11/011,557
; PRIORITY FILING DATE: 2004-12-13
; PRIOR APPLICATION NUMBER: 60/529,223
; NUMBER OF SEQ ID NOS: 97
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 79
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Alternative pseudo-epsilon RACK peptide
US-11-011-557-79

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```

Query Match      83.3%; Score 40; DB 6; Length 8;
Best Local Similarity 87.5%; Pred. No. 1.7e+06;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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```

QY      1 HDAPIGYD 8
        |||||
Db      1 HDAPIDPYD 8

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RESULT 33
US-10-437-963-131067
; Sequence 131067, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barzak, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; PRIORITY FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 131067
; LENGTH: 586
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_33169C.1.pep

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US-10-437-963-131067
Query Match      81.2%; Score 39; DB 4; Length 586;
Best Local Similarity 75.0%; Pred. No. 62;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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QY      1 HDAPIGYD 8
        |||||
Db      408 HDVPIGHD 415

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RESULT 34
US-10-437-963-172827
; Sequence 172827, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barzak, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; PRIORITY FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 172827
; LENGTH: 719
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_70925C.1.pep
US-10-437-963-172827

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Query Match      81.2%; Score 39; DB 4; Length 719;
Best Local Similarity 85.7%; Pred. No. 76;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      2 DAPIGYD 8
        |||||
Db      553 DAPVGYD 559

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RESULT 35
US-11-011-557-6
; Sequence 6, Application US/11011557
; Publication No. US20050187156A1
; GENERAL INFORMATION:
; APPLICANT: Mochly-Rosen, Daria
; APPLICANT: Chen, Leon E.
; TITLE OF INVENTION: Isozyme-Specific Antagonists of Protein Kinase C
; FILE REFERENCE: 58600-8212.US00
; CURRENT APPLICATION NUMBER: US/11/011,557
; PRIORITY FILING DATE: 2004-12-13
; PRIOR APPLICATION NUMBER: 60/529,223
; NUMBER OF SEQ ID NOS: 97
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 6
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-011-557-6

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```

Query Match      79.2%; Score 38; DB 6; Length 8;
Best Local Similarity 62.5%; Pred. No. 1.7e+06;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

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```

QY      1 HDAPIGYD 8

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Db 1 HETPLGYD 8

RESULT 36
US-11-011-557-96
; Sequence 96, Application US/11011557
; Publication No. US20050187156A1
; GENERAL INFORMATION:
; APPLICANT: Mochly-Rosen, Daria
; APPLICANT: Chen, Leon E.
; TITLE OF INVENTION: Isozyme-Specific Antagonists of Protein Kinase C
; FILE REFERENCE: 58600-8212.US00
; CURRENT FILING DATE: 2004-12-13
; PRIOR APPLICATION NUMBER: 60/529,223
; PRIOR FILING DATE: 2003-12-11
; NUMBER OF SEQ ID NOS: 97
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 96
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-011-557-96

Query Match 79.2% Score 38; DB 6; Length 18;
Best Local Similarity 62.5% Pred. No. 2.6;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 HDAPIGYD 8
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Db 6 HETPLGYD 13

RESULT 37
US-10-199-820-290
; Sequence 290, Application US/10199820
; Publication No. US20030180739A1
; GENERAL INFORMATION:
; APPLICANT: Board of Trustees of the University of Illinois
; APPLICANT: Priliano, Thomas
; APPLICANT: Chang, Bey-din
; APPLICANT: Robinson, Igor
; TITLE OF INVENTION: Methods and Reagents for Identifying Gene Targets for Treating Ca
; FILE REFERENCE: 99,216-U
; CURRENT APPLICATION NUMBER: US/10/199,820
; CURRENT FILING DATE: 2002-09-23
; NUMBER OF SEQ ID NOS: 314
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 290
; LENGTH: 35
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-199-820-290

Query Match 79.2% Score 38; DB 4; Length 35;
Best Local Similarity 62.5% Pred. No. 5.2;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 HDAPIGYD 8
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Db 16 HETPLGYD 23

RESULT 38
US-10-424-599-182799
; Sequence 182799, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei

; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 182799
; LENGTH: 145
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURES:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_136081C.1.pep
US-10-424-599-182799

Query Match 79.2% Score 38; DB 4; Length 145;
Best Local Similarity 71.4% Pred. No. 23;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 HDAPIGY 7
||:||||
Db 4 HDSPVGY 10

RESULT 39
US-10-466-162-4
; Sequence 4, Application US/10466162
; Publication No. US20050170343A1
; GENERAL INFORMATION:
; APPLICANT: EXELIXIS, INC.
; TITLE OF INVENTION: Modulating Insulin Receptor Signaling
; FILE REFERENCE: EX02-001C-PC
; CURRENT APPLICATION NUMBER: US/10/466,162
; CURRENT FILING DATE: 2003-07-11
; PRIOR APPLICATION NUMBER: US 60/261,335
; PRIOR FILING DATE: 2001-01-12
; PRIOR APPLICATION NUMBER: US 60/261,694
; PRIOR FILING DATE: 2001-01-12
; PRIOR APPLICATION NUMBER: US 60/261,532
; PRIOR FILING DATE: 2001-01-12
; PRIOR APPLICATION NUMBER: US 60/261,361
; PRIOR FILING DATE: 2001-01-12
; PRIOR APPLICATION NUMBER: US 60/261,531
; PRIOR FILING DATE: 2001-01-12
; PRIOR APPLICATION NUMBER: US 60/261,457
; PRIOR FILING DATE: 2001-01-12
; PRIOR APPLICATION NUMBER: US 60/261,226
; PRIOR FILING DATE: 2001-01-12
; PRIOR APPLICATION NUMBER: US 60/261,304
; PRIOR FILING DATE: 2001-01-12
; PRIOR APPLICATION NUMBER: US 60/261,459
; PRIOR FILING DATE: 2001-01-12
; PRIOR APPLICATION NUMBER: US 60/261,456
; PRIOR FILING DATE: 2001-01-12
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 76
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 682
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-466-162-4

Query Match 79.2% Score 38; DB 5; Length 682;
Best Local Similarity 62.5% Pred. No. 1.1e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 HDAPIGYD 8
||:||||
Db 88 HETPLGYD 95

RESULT 40
US-10-618-941-72

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; Sequence 72, Application US/10618941
; Publication No. US20040197792A1
; GENERAL INFORMATION:
; APPLICANT: WHYTE, DAVID
; APPLICANT: MANNING, GERARD
; APPLICANT: CAENEPEEL, SEAN
; TITLE OF INVENTION: NOVEL KINASES
; FILE REFERENCE: 034536-0321
; CURRENT APPLICATION NUMBER: US/10/618,941
; CURRENT FILING DATE: 2003-07-15
; PRIOR APPLICATION NUMBER: 60/395,632
; PRIOR FILING DATE: 2002-07-15
; NUMBER OF SEQ ID NOS: 143
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 72
; LENGTH: 683
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-618-941-72
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Query Match 79.2%; Score 38; DB 4; Length 683;
Best Local Similarity 62.5%; Pred. No. 1.1e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
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QY 1 HDAPIGYD 8
|:|:|
Db 88 HETPLGYD 95
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Job time : 165 secs
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November 2005

Published_Applications Nucleic Acid and Published_Applications Amino Acid database searches now generate two sets of results each. The Published_Applications databases have been split into two parts to reduce the amount of time required for their daily updates. This results in more machine time being available for processing searches.

Newly published applications will appear in the Published_Applications_New databases; older published applications make up the Published_Applications_Main databases.

Searches run against Nucleic Acid Published_Applications produce two sets of results, with the extensions **.rnpbm** (Published_Applications_NA_Main) and **.rnpbn** (Published_Applications_NA_New).

Searches run against Amino Acid Published_Applications produce two sets of results, with the extensions **.rapbm** (Published_Applications_AA_Main) and **.rapbn** (Published_Applications_AA_New).

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GenCore version 5.1.6
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OM protein - protein search, using sw model1

Run on: December 3, 2005, 23:29:20 ; Search time 11 Seconds
(without alignments)
3.482 Million cell updates/sec

Title: US-10-807-553-2

Perfect score: 48

Sequence: 1 HDAPICVD 8

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 26661 seqs, 4788334 residues

26661

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : Published Applications AA New:*

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*Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed.
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	70.8	485	6	US-10-467-657-2498	Sequence 2498, Ap
2	68.8	164	6	US-10-467-657-2912	Sequence 2912, Ap
3	68.8	719	6	US-10-467-657-762	Sequence 762, App
4	66.7	102	6	US-10-816-768-45	Sequence 45, Appl
5	66.7	595	6	US-10-510-386-240	Sequence 240, App
6	64.6	496	7	US-11-067-121-3	Sequence 3, Appli
7	62.5	496	7	US-11-067-121-12	Sequence 12, Appl
8	62.5	659	6	US-10-467-657-6006	Sequence 6006, Ap
9	61.5	199	6	US-10-467-657-2460	Sequence 2460, Ap
10	60.4	150	7	US-11-074-176-102	Sequence 102, App
11	60.4	417	6	US-10-971-560-4	Sequence 4, Appli
12	60.4	494	6	US-10-971-560-7	Sequence 7, Appli
13	60.4	501	6	US-10-971-560-2	Sequence 2, Appli
14	60.4	501	6	US-10-971-560-10	Sequence 10, Appl
15	60.4	501	6	US-11-067-121-1	Sequence 1, Appli
16	60.4	530	6	US-10-980-388-62	Sequence 62, Appl
17	58.3	284	7	US-11-055-822-692	Sequence 692, App
18	58.3	284	7	US-11-055-822-770	Sequence 770, App
19	58.3	310	6	US-10-467-657-7412	Sequence 7412, Ap
20	58.3	326	6	US-10-793-626-254	Sequence 254, App
21	58.3	480	6	US-10-510-386-12	Sequence 12, Appl
22	58.3	674	6	US-10-467-657-6812	Sequence 6812, Ap
23	57.3	433	6	US-10-667-295-83	Sequence 83, Appl
24	57.3	434	6	US-10-667-295-141	Sequence 141, Appl
25	57.3	505	6	US-10-667-295-82	Sequence 82, Appl

26	27.5	57.3	506	6	US-10-667-295-140	Sequence 140, App
27	27.5	57.3	526	6	US-10-667-295-139	Sequence 139, Appl
28	27.5	57.3	534	6	US-10-667-295-81	Sequence 81, Appl
29	27	56.2	54	6	US-10-467-657-412	Sequence 412, App
30	27	56.2	92	6	US-10-467-657-3158	Sequence 3158, App
31	27	56.2	405	6	US-10-467-657-2310	Sequence 2310, Ap
32	27	56.2	413	6	US-10-467-657-1858	Sequence 1858, Ap
33	27	56.2	435	6	US-10-467-657-4570	Sequence 4570, Ap
34	27	56.2	443	6	US-10-793-626-1200	Sequence 1200, Ap
35	27	56.2	528	6	US-10-467-657-6146	Sequence 6146, Ap
36	27	56.2	534	6	US-10-467-657-468	Sequence 468, App
37	27	56.2	611	7	US-11-082-389-436	Sequence 436, App
38	27	56.2	680	6	US-10-467-657-2008	Sequence 2008, App
39	27	56.2	756	6	US-10-467-657-8694	Sequence 8694, App
40	27	56.2	872	6	US-10-467-657-78	Sequence 78, Appl
41	27	56.2	886	6	US-10-467-657-4544	Sequence 4544, Ap
42	27	56.2	1388	6	US-10-821-334-1143	Sequence 1143, Ap
43	27	56.2	1560	7	US-11-059-982-1	Sequence 1, Appli
44	26	54.2	18	6	US-10-416-384-12	Sequence 12, Appl
45	26	54.2	148	6	US-10-512-109-19	Sequence 19, Appl
46	26	54.2	148	6	US-10-512-109-21	Sequence 21, Appl
47	26	54.2	182	6	US-10-467-657-8302	Sequence 8302, Ap
48	26	54.2	195	7	US-11-132-839-11	Sequence 11, Appl
49	26	54.2	203	7	US-11-132-839-10	Sequence 10, Appl
50	26	54.2	211	7	US-11-132-839-12	Sequence 12, Appl
51	26	54.2	228	6	US-10-848-689-1	Sequence 1, Appli
52	26	54.2	243	6	US-10-131-826A-362	Sequence 362, App
53	26	54.2	243	6	US-10-512-109-23	Sequence 23, Appl
54	26	54.2	243	6	US-10-512-109-48	Sequence 48, Appl
55	26	54.2	244	6	US-10-793-626-994	Sequence 994, Appl
56	26	54.2	245	6	US-10-793-626-2916	Sequence 2916, App
57	26	54.2	248	7	US-11-082-389-438	Sequence 438, App
58	26	54.2	282	6	US-10-467-657-5450	Sequence 5450, Ap
59	26	54.2	280	7	US-11-054-515-3231	Sequence 3231, Ap
60	26	54.2	282	6	US-10-467-657-5564	Sequence 5564, App
61	26	54.2	306	7	US-11-017-550-43	Sequence 43, Appl
62	26	54.2	309	7	US-11-065-669-2	Sequence 2, Appli
63	26	54.2	309	7	US-11-054-515-3230	Sequence 3230, Ap
64	26	54.2	341	6	US-10-821-334-1628	Sequence 1628, Ap
65	26	54.2	352	7	US-11-108-528-20	Sequence 20, Appl
66	26	54.2	352	7	US-11-108-528-22	Sequence 22, Appl
67	26	54.2	360	6	US-10-793-626-2150	Sequence 2150, App
68	26	54.2	376	6	US-10-793-626-2106	Sequence 2106, App
69	26	54.2	386	7	US-11-055-822-586	Sequence 586, App
70	26	54.2	499	6	US-10-467-657-2096	Sequence 2096, App
71	26	54.2	500	6	US-10-467-657-594	Sequence 594, App
72	26	54.2	544	6	US-10-467-657-2436	Sequence 2436, App
73	26	54.2	552	7	US-11-074-176-204	Sequence 204, App
74	26	54.2	589	6	US-10-467-657-4826	Sequence 4826, App
75	26	54.2	675	6	US-10-467-657-3802	Sequence 3802, App
76	26	54.2	687	6	US-10-485-517-274	Sequence 274, App
77	26	54.2	720	7	US-11-102-240-38	Sequence 38, Appl
78	26	54.2	735	6	US-10-467-657-1536	Sequence 1536, App
79	26	54.2	747	7	US-11-182-592-2	Sequence 2, Appli
80	26	54.2	787	6	US-10-467-657-2832	Sequence 2832, App
81	26	54.2	855	6	US-10-501-039-4	Sequence 4, Appli
82	26	54.2	865	6	US-10-457-962B-33	Sequence 33, Appl
83	26	54.2	1238	7	US-11-078-735-21	Sequence 21, Appl
84	26	54.2	1432	6	US-10-510-386-218	Sequence 218, App
85	26	54.2	1437	7	US-11-074-176-96	Sequence 96, Appl
86	25.5	53.1	334	7	US-11-055-822-24	Sequence 24, Appl
87	25	52.1	20	7	US-11-054-515-2520	Sequence 2500, App
88	25	52.1	21	6	US-10-939-890-526	Sequence 526, App
89	25	52.1	21	6	US-10-939-890-578	Sequence 578, App
90	25	52.1	97	6	US-10-821-334-1132	Sequence 1132, App
91	25	52.1	94	7	US-11-055-822-86	Sequence 86, Appl
92	25	52.1	124	6	US-10-467-657-1132	Sequence 1132, App
93	25	52.1	143	6	US-10-793-626-1838	Sequence 1838, App
94	25	52.1	143	6	US-10-793-626-1940	Sequence 1940, App
95	25	52.1	149	6	US-10-467-657-2862	Sequence 2862, App
96	25	52.1	152	6	US-10-957-569-38	Sequence 38, Appl
97	25	52.1	183	6	US-10-467-657-8825	Sequence 8825, App
98	25	52.1	183	7	US-11-055-822-84	Sequence 84, Appl

99 25 52.1 252 7 US-11-054-515-1416
100 25 52.1 287 7 US-11-055-822-102

Sequence 1416, Ap
Sequence 102, App

ALIGNMENTS

RESULT 1

US-10-467-657-2498
; Sequence 2498, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SPA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: Seqwin99, version 1.04
; SEQ ID NO 2498
; LENGTH: 485
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-2498

Query Match 70.8%; Score 34; DB 6; Length 485;
Best Local Similarity 85.7%; Pred. No. 5.6;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 HDAPIGY 7
DB 226 HDASIGY 232

RESULT 2

US-10-467-657-2912
; Sequence 2912, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SPA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: Seqwin99, version 1.04
; SEQ ID NO 2912
; LENGTH: 164
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-2912

Query Match 68.8%; Score 33; DB 6; Length 164;
Best Local Similarity 83.3%; Pred. No. 2.8;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 APIGYD 8
DB 47 APIGYD 52

RESULT 3

US-10-467-657-762
; Sequence 762, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SPA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: Seqwin99, version 1.04
; SEQ ID NO 762
; LENGTH: 719
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-762

Query Match 68.8%; Score 33; DB 6; Length 719;
Best Local Similarity 83.3%; Pred. No. 1.4;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 DAPIGY 7
DB 299 DAPIGY 304

RESULT 4

US-10-816-768-45
; Sequence 45, Application US/10816768
; Publication No. US20050250936A1
; GENERAL INFORMATION:
; APPLICANT: Oppermann, Hermann
; APPLICANT: Tai, Mei-Sheng
; APPLICANT: McCartney, John
; TITLE OF INVENTION: Modified TGF-beta Superfamily Proteins
; FILE REFERENCE: STR-075
; CURRENT APPLICATION NUMBER: US/10/816,768
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 124
; SOFTWARE: PatentIn version 2.0
; SEQ ID NO 45
; LENGTH: 102
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; FEATURE:
; OTHER INFORMATION: DPP
US-10-816-768-45

Query Match 66.7%; Score 32; DB 6; Length 102;
Best Local Similarity 83.3%; Pred. No. 2.6;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 APIGYD 8
DB 21 APIGYD 26

RESULT 5

US-10-510-386-240
; Sequence 240, Application US/10510386
; Publication No. US20050244922A1
; GENERAL INFORMATION:
; APPLICANT: Andersen, Jens Tonne
; APPLICANT: Clausen, Ib Groth
; APPLICANT: Jorgensen, Steen Troels
; APPLICANT: Olsen, Peter Bjarke

```
; APPLICANT: Raasmussen, Michael Dolberg
; TITLE OF INVENTION: Improved Bacillus Host Cell
; FILE REFERENCE: 10294-204-US
; CURRENT APPLICATION NUMBER: US/10/510,386
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 248
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 240
; LENGTH: 595
; TYPE: PRT
; ORGANISM: Bacillus licheniformis
US-10-510-386-240
```

```
Query Match      66.7%; Score 32; DB 6; Length 595;
Best Local Similarity 62.5%; Pred. No. 18;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      1 HDAPIGYD 8
      |||:|
Db      284 HNAFLPYD 291
```

```
RESULT 6
US-11-067-121-3
; Sequence 3, Application US/11067121
; Publication No. US20050261185A1
; GENERAL INFORMATION:
; APPLICANT: Martijn, Cecile
; APPLICANT: Rondahl, Lena
; TITLE OF INVENTION: THERAPEUTIC PROTEINS
; FILE REFERENCE: 18909-002001
; CURRENT APPLICATION NUMBER: US/11/067,121
; CURRENT FILING DATE: 2005-02-25
; PRIOR APPLICATION NUMBER: US 60/576,445
; PRIOR FILING DATE: 2004-06-02
; PRIOR APPLICATION NUMBER: SE 0400489-1
; PRIOR FILING DATE: 2004-02-27
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 496
; TYPE: PRT
; ORGANISM: Mus musculus
US-11-067-121-3
```

```
Query Match      64.6%; Score 31; DB 7; Length 496;
Best Local Similarity 71.4%; Pred. No. 23;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      2 DAPIGYD 8
      |||:|
Db      68 DAPLDYD 74
```

```
RESULT 7
US-11-067-121-12
; Sequence 12, Application US/11067121
; Publication No. US20050261185A1
; GENERAL INFORMATION:
; APPLICANT: Martijn, Cecile
; APPLICANT: Rondahl, Lena
; TITLE OF INVENTION: THERAPEUTIC PROTEINS
; FILE REFERENCE: 18909-002001
; CURRENT APPLICATION NUMBER: US/11/067,121
; CURRENT FILING DATE: 2005-02-25
; PRIOR APPLICATION NUMBER: US 60/576,445
; PRIOR FILING DATE: 2004-06-02
; PRIOR APPLICATION NUMBER: SE 0400489-1
; PRIOR FILING DATE: 2004-02-27
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 496
```

```
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-067-121-12
```

```
Query Match      62.5%; Score 30; DB 7; Length 496;
Best Local Similarity 71.4%; Pred. No. 37;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      2 DAPIGYD 8
      |||:|
Db      68 DAPLDYD 74
```

```
RESULT 8
US-10-467-657-6006
; Sequence 6006, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SPA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASTIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 6006
; LENGTH: 659
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-6006
```

```
Query Match      62.5%; Score 30; DB 6; Length 659;
Best Local Similarity 62.5%; Pred. No. 50;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
```

```
QY      1 HDAPIGYD 8
      |||:|
Db      258 HGAFLGAD 265
```

```
RESULT 9
US-10-467-657-2460
; Sequence 2460, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SPA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASTIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 2460
; LENGTH: 199
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-2460
```

```
Query Match      61.5%; Score 29.5; DB 6; Length 199;
Best Local Similarity 46.2%; Pred. No. 17;
Matches 6; Conservative 1; Mismatches 1; Indels 5; Gaps 1;
```

OY 1 HDAP1-----GYD 8
|||
Db 148 HDTPLGONGFGYD 160

RESULT 10
US-11-074-176-102
; Sequence 102, Application US/11074176
; Publication No. US20050250135A1
; GENERAL INFORMATION:
; APPLICANT: Kjaerhammer, Todd R.
; APPLICANT: Russell, William M.
; APPLICANT: Altermann, Eric
; APPLICANT: McCalliffe, Olivia
; APPLICANT: Perill, Andrea Azcarate
; TITLE OF INVENTION: Nucleic Acid Sequences Encoding
; TITLE OF INVENTION: Stress-Related Proteins and Uses Therefore
; FILE REFERENCE: 5051-694
; CURRENT FILING DATE: 2005-03-07
; PRIOR APPLICATION NUMBER: 60/551,161
; PRIOR FILING DATE: 2004-03-08
; NUMBER OF SEQ ID NOS: 381
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 102
; LENGTH: 150
; TYPE: PRT
; ORGANISM: Lactobacillus acidophilus
US-11-074-176-102

Query Match 60.4%; Score 29; DB 7; Length 150;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 HDAP1 5
|||
Db 140 HDAP1 144

RESULT 11
US-10-971-560-4
; Sequence 4, Application US/10971560
; Publication No. US20050244842A1
; GENERAL INFORMATION:
; APPLICANT: Enerbck, Sven
; APPLICANT: Krook, Katarina
; APPLICANT: Rondahl, Lena
; APPLICANT: Wasserman, Wyeth
; TITLE OF INVENTION: PROMOTER SEQUENCES
; FILE REFERENCE: 13425-042001
; CURRENT APPLICATION NUMBER: US/10/971,560
; CURRENT FILING DATE: 2004-10-22
; PRIOR APPLICATION NUMBER: US/09/963,285
; PRIOR FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: SE 0004102-0
; PRIOR FILING DATE: 2000-11-09
; PRIOR APPLICATION NUMBER: US 60/238,897
; PRIOR FILING DATE: 2000-10-10
; PRIOR APPLICATION NUMBER: SE 0003435-5
; PRIOR FILING DATE: 2000-09-26
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 417
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-971-560-4

Query Match 60.4%; Score 29; DB 6; Length 417;
Best Local Similarity 62.5%; Pred. No. 49;
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 HDAP1GYD 8
|||
Db 406 HAAFYSD 413

RESULT 12
US-10-971-560-7
; Sequence 7, Application US/10971560
; Publication No. US20050244842A1
; GENERAL INFORMATION:
; APPLICANT: Enerbck, Sven
; APPLICANT: Krook, Katarina
; APPLICANT: Rondahl, Lena
; APPLICANT: Wasserman, Wyeth
; TITLE OF INVENTION: PROMOTER SEQUENCES
; FILE REFERENCE: 13425-042001
; CURRENT APPLICATION NUMBER: US/10/971,560
; CURRENT FILING DATE: 2004-10-22
; PRIOR APPLICATION NUMBER: US/09/963,285
; PRIOR FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: SE 0004102-0
; PRIOR FILING DATE: 2000-11-09
; PRIOR APPLICATION NUMBER: US 60/238,897
; PRIOR FILING DATE: 2000-10-10
; PRIOR APPLICATION NUMBER: SE 0003435-5
; PRIOR FILING DATE: 2000-09-26
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 494
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-971-560-7

Query Match 60.4%; Score 29; DB 6; Length 494;
Best Local Similarity 62.5%; Pred. No. 58;
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
OY 1 HDAP1GYD 8
|||
Db 483 HAAFYSD 490

RESULT 13
US-10-971-560-2
; Sequence 2, Application US/10971560
; Publication No. US20050244842A1
; GENERAL INFORMATION:
; APPLICANT: Enerbck, Sven
; APPLICANT: Krook, Katarina
; APPLICANT: Rondahl, Lena
; APPLICANT: Wasserman, Wyeth
; TITLE OF INVENTION: PROMOTER SEQUENCES
; FILE REFERENCE: 13425-042001
; CURRENT APPLICATION NUMBER: US/10/971,560
; CURRENT FILING DATE: 2004-10-22
; PRIOR APPLICATION NUMBER: US/09/963,285
; PRIOR FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: SE 0004102-0
; PRIOR FILING DATE: 2000-11-09
; PRIOR APPLICATION NUMBER: US 60/238,897
; PRIOR FILING DATE: 2000-10-10
; PRIOR APPLICATION NUMBER: SE 0003435-5
; PRIOR FILING DATE: 2000-09-26
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 501
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-971-560-2

Query Match 60.4%; Score 29; DB 6; Length 501;

Best Local Similarity 62.5%; Pred. No. 59;
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 HDAPIGYD 8
Db 490 HAAPYSYD 497

RESULT 14

US-10-971-560-10
; Sequence 10, Application US/10971560
; Publication No. US20050244842A1
; GENERAL INFORMATION:
; APPLICANT: Enerbeck, Sven
; APPLICANT: Krook, Katarina
; APPLICANT: Rondahl, Lena
; APPLICANT: Wasserman, Wyeth
; TITLE OF INVENTION: PROMOTER SEQUENCES
; FILE REFERENCE: 13425-04201
; CURRENT APPLICATION NUMBER: US/10/971,560
; CURRENT FILING DATE: 2004-10-22
; PRIOR APPLICATION NUMBER: US/09/963,285
; PRIOR FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: SE 0004102-0
; PRIOR FILING DATE: 2000-11-09
; PRIOR APPLICATION NUMBER: US 60/238,897
; PRIOR FILING DATE: 2000-10-10
; PRIOR APPLICATION NUMBER: SE 0003435-5
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 501
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-971-560-10

Query Match 60.4%; Score 29; DB 6; Length 501;
Best Local Similarity 62.5%; Pred. No. 59;
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 HDAPIGYD 8
Db 490 HAAPYSYD 497

RESULT 15
US-11-067-121-1
; Sequence 1, Application US/11067121
; Publication No. US2005026185A1
; GENERAL INFORMATION:
; APPLICANT: Martijn, Cecile
; APPLICANT: Rondahl, Lena
; TITLE OF INVENTION: THERAPEUTIC PROTEINS
; FILE REFERENCE: 18909-002001
; CURRENT APPLICATION NUMBER: US/11/067,121
; CURRENT FILING DATE: 2005-02-25
; PRIOR APPLICATION NUMBER: US 60/576,445
; PRIOR FILING DATE: 2004-06-02
; PRIOR APPLICATION NUMBER: SE 0400489-1
; PRIOR FILING DATE: 2004-02-27
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 501
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-067-121-1

Query Match 60.4%; Score 29; DB 7; Length 501;
Best Local Similarity 62.5%; Pred. No. 59;
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 HDAPIGYD 8
Db 490 HAAPYSYD 497

RESULT 16
US-10-980-388-62
; Sequence 62, Application US/10980388
; Publication No. US20050255490A1
; GENERAL INFORMATION:
; APPLICANT: Vogel, Gabriel
; APPLICANT: Parodi, Luis A.
; APPLICANT: Hiesch, Ronald R.
; APPLICANT: Lind, Peter
; APPLICANT: Kayes, Paul S.
; APPLICANT: Ruff, Valerie
; APPLICANT: Huff, Rita M.
; APPLICANT: Wood, Linda S.
; TITLE OF INVENTION: Novel G Protein-Coupled Receptors Cross-Reference To Related Appl.
; FILE REFERENCE: 00325 US1
; CURRENT APPLICATION NUMBER: US/10/980,388
; CURRENT FILING DATE: 2004-11-02
; PRIOR APPLICATION NUMBER: US/09/791,932
; PRIOR FILING DATE: 2001-02-23
; PRIOR APPLICATION NUMBER: 60/184,305
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/184,304
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/184,303
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/184,397
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/184,247
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/188,880
; PRIOR FILING DATE: 2000-03-13
; PRIOR APPLICATION NUMBER: 60/217,369
; PRIOR FILING DATE: 2000-07-11
; PRIOR APPLICATION NUMBER: 60/217,370
; PRIOR FILING DATE: 2000-07-11
; PRIOR APPLICATION NUMBER: 60/218,492
; PRIOR FILING DATE: 2000-07-20
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 184
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 62
; LENGTH: 530
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-980-388-62

Query Match 60.4%; Score 29; DB 6; Length 530;
Best Local Similarity 66.7%; Pred. No. 63;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HDAPIG 6
Db 521 HEAPLG 526

RESULT 17
US-11-055-822-692
; Sequence 692, Application US/11055822
; Publication No. US20050260707A1
; GENERAL INFORMATION:
; APPLICANT: Pompejus, Markus
; APPLICANT: Kroger, Burkhard
; APPLICANT: Schroder, Hartwig
; APPLICANT: Zelder, Oskar
; APPLICANT: Heberhauser, Gregor
; TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING
; FILE REFERENCE: BGI-121CPCN

```
; CURRENT APPLICATION NUMBER: US/11/055,822
; CURRENT FILING DATE: 2005-02-11
; PRIOR APPLICATION NUMBER: 09/606,740
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: 60/141,031
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: 60/142,101
; PRIOR FILING DATE: 1999-07-02
; PRIOR APPLICATION NUMBER: 60/148,613
; PRIOR FILING DATE: 1999-08-12
; PRIOR APPLICATION NUMBER: 60/187,970
; PRIOR FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: DE 19930476.9
; PRIOR FILING DATE: 1999-07-01
; PRIOR APPLICATION NUMBER: DE 19931415.2
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931418.7
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931419.5
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931420.9
; PRIOR FILING DATE: 1999-07-08
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1158
; SEQ ID NO 692
; LENGTH: 284
; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-11-055-822-692
```

```
Query Match          58.3%; Score 28; DB 7; Length 284;
Best Local Similarity 50.0%; Pred. No. 51;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
```

```
Oy      1 HDAPIGVD 8
Db      261 HDVPSRD 268
```

```
RESULT 18
US-11-055-822-770
; Sequence 770, Application US/11055822
; Publication No. US20050260707A1
; GENERAL INFORMATION:
; APPLICANT: Pompeju, Markus
; APPLICANT: Kroeger, Burkhard
; APPLICANT: Schroder, Hartwig
; APPLICANT: Zelder, Oskar
; APPLICANT: Habermann, Gregor
; TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING
; TITLE OF INVENTION: METABOLIC PATHWAY PROTEINS
; FILE REFERENCE: BGI-121PCN
; CURRENT APPLICATION NUMBER: US/11/055,822
; CURRENT FILING DATE: 2005-02-11
; PRIOR APPLICATION NUMBER: 09/606,740
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: 60/141,031
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: 60/142,101
; PRIOR FILING DATE: 1999-07-02
; PRIOR APPLICATION NUMBER: 60/148,613
; PRIOR FILING DATE: 1999-08-12
; PRIOR APPLICATION NUMBER: 60/187,970
; PRIOR FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: DE 19930476.9
; PRIOR FILING DATE: 1999-07-01
; PRIOR APPLICATION NUMBER: DE 19931415.2
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931418.7
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931419.5
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931420.9
```

```
; PRIOR FILING DATE: 1999-07-08
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1158
; SEQ ID NO 770
; LENGTH: 284
; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-11-055-822-770
```

```
Query Match          58.3%; Score 28; DB 7; Length 284;
Best Local Similarity 50.0%; Pred. No. 51;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
```

```
Oy      1 HDAPIGVD 8
Db      261 HDVPSRD 268
```

```
RESULT 19
US-10-467-657-7412
; Sequence 7412, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SPA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 7412
; LENGTH: 310
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-7412
```

```
Query Match          58.3%; Score 28; DB 6; Length 310;
Best Local Similarity 71.4%; Pred. No. 56;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
Oy      1 HDAPIGV 7
Db      3 HIPPIGY 9
```

```
RESULT 20
US-10-793-626-254
; Sequence 254, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PUS480US
; CURRENT APPLICATION NUMBER: US/10/793,626
; CURRENT FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 254
; LENGTH: 326
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: amino acid sequence
US-10-793-626-254
```

Query Match 58.3%; Score 28; DB 6; Length 326;
Best Local Similarity 83.3%; Pred. No. 59;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 DAPIGY 7
Db 187 DFIGY 192

RESULT 21
US-10-510-386-12
; Sequence 12, Application US/10510386
; Publication No. US20050244922A1
; GENERAL INFORMATION:
; APPLICANT: Andersen, Jens Tonne
; APPLICANT: Clausen, Ib Groth
; APPLICANT: Jorgensen, Steen Troels
; APPLICANT: Olsen, Peter Bjarke
; APPLICANT: Rasmussen, Michael Dolberg
; TITLE OF INVENTION: Improved Bacillus Host Cell
; FILE REFERENCE: 10294.204-US
; CURRENT APPLICATION NUMBER: US/10/510.386
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 248
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 12
; LENGTH: 480
; TYPE: PRT
; ORGANISM: Bacillus licheniformis
US-10-510-386-12

Query Match 58.3%; Score 28; DB 6; Length 480;
Best Local Similarity 66.7%; Pred. No. 90;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 DAPIGY 7
Db 210 DKPGY 215

RESULT 22
US-10-467-657-8812
; Sequence 6812, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SPA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467.657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 6812
; LENGTH: 674
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-8812

Query Match 58.3%; Score 28; DB 6; Length 674;
Best Local Similarity 57.1%; Pred. No. 1.3e+02;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 HDAPGY 7
Db 111 HDKRGY 117

RESULT 23
US-10-667-295-83

; Sequence 83, Application US/10667295
; Publication No. US20050257293A1
; GENERAL INFORMATION:
; APPLICANT: Mascia, Peter
; TITLE OF INVENTION: BIOLOGICAL CONTAINMENT SYSTEM
; FILE REFERENCE: 11696-047001
; CURRENT APPLICATION NUMBER: US/10/667,295
; CURRENT FILING DATE: 2003-09-17
; PRIOR APPLICATION NUMBER: US 60/411,823
; PRIOR FILING DATE: 2002-09-17
; NUMBER OF SEQ ID NOS: 263
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 83
; LENGTH: 433
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)...(433)
; OTHER INFORMATION: Ceres Seq. ID no. 12558792
US-10-667-295-83

Query Match 57.3%; Score 27.5; DB 6; Length 433;
Best Local Similarity 66.7%; Pred. No. 1e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 1; Gaps 1;

QY 1 HDAPY-GYD 8
Db 309 HDKLGVD 317

RESULT 24
US-10-667-295-141
; Sequence 141, Application US/10667295
; Publication No. US20050257293A1
; GENERAL INFORMATION:
; APPLICANT: Mascia, Peter
; TITLE OF INVENTION: BIOLOGICAL CONTAINMENT SYSTEM
; FILE REFERENCE: 11696-047001
; CURRENT APPLICATION NUMBER: US/10/667,295
; CURRENT FILING DATE: 2003-09-17
; PRIOR APPLICATION NUMBER: US 60/411,823
; PRIOR FILING DATE: 2002-09-17
; NUMBER OF SEQ ID NOS: 263
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 141
; LENGTH: 434
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)...(434)
; OTHER INFORMATION: Ceres Seq. ID no. 13531808
US-10-667-295-141

Query Match 57.3%; Score 27.5; DB 6; Length 434;
Best Local Similarity 66.7%; Pred. No. 1e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 1; Gaps 1;

QY 1 HDAPY-GYD 8
Db 310 HDKLGVD 318

RESULT 25
US-10-667-295-82
; Sequence 82, Application US/10667295
; Publication No. US20050257293A1
; GENERAL INFORMATION:
; APPLICANT: Mascia, Peter

```
; TITLE OF INVENTION: BIOLOGICAL CONTAINMENT SYSTEM
; FILE REFERENCE: 11696-047001
; CURRENT APPLICATION NUMBER: US/10/667,295
; CURRENT FILING DATE: 2003-09-17
; PRIOR APPLICATION NUMBER: US 60/411,823
; PRIOR FILING DATE: 2002-09-17
; NUMBER OF SEQ ID NOS: 263
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 82
; LENGTH: 505
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)...(505)
; OTHER INFORMATION: Ceres Seq. ID no. 12558791
US-10-667-295-82
```

```
Query Match      57.3%; Score 27.5; DB 6; Length 505;
Best Local Similarity 66.7%; Pred. No. 1.2e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 1; Gaps 1;
```

```
OY      1 HDAP1-GYD 8
        ||| : |||
Db      381 HDAKLAGYD 389
```

```
RESULT 26
US-10-667-295-140
; Sequence 140, Application US/10667295
; Publication No. US20050257293A1
; GENERAL INFORMATION:
; APPLICANT: Masclia, Peter
; TITLE OF INVENTION: BIOLOGICAL CONTAINMENT SYSTEM
; FILE REFERENCE: 11696-047001
; CURRENT APPLICATION NUMBER: US/10/667,295
; CURRENT FILING DATE: 2003-09-17
; PRIOR APPLICATION NUMBER: US 60/411,823
; PRIOR FILING DATE: 2002-09-17
; NUMBER OF SEQ ID NOS: 263
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 140
; LENGTH: 506
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)...(506)
; OTHER INFORMATION: Ceres Seq. ID no. 13531807
US-10-667-295-140
```

```
Query Match      57.3%; Score 27.5; DB 6; Length 506;
Best Local Similarity 66.7%; Pred. No. 1.2e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 1; Gaps 1;
```

```
OY      1 HDAP1-GYD 8
        ||| : |||
Db      382 HDAKLAGYD 390
```

```
RESULT 27
US-10-667-295-139
; Sequence 139, Application US/10667295
; Publication No. US20050257293A1
; GENERAL INFORMATION:
; APPLICANT: Masclia, Peter
; TITLE OF INVENTION: BIOLOGICAL CONTAINMENT SYSTEM
; FILE REFERENCE: 11696-047001
; CURRENT APPLICATION NUMBER: US/10/667,295
; CURRENT FILING DATE: 2003-09-17
; PRIOR APPLICATION NUMBER: US 60/411,823
; PRIOR FILING DATE: 2002-09-17
; NUMBER OF SEQ ID NOS: 263
```

```
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 139
; LENGTH: 526
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)...(526)
; OTHER INFORMATION: Ceres Seq. ID no. 13531806
US-10-667-295-139
```

```
Query Match      57.3%; Score 27.5; DB 6; Length 526;
Best Local Similarity 66.7%; Pred. No. 1.3e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 1; Gaps 1;
```

```
OY      1 HDAP1-GYD 8
        ||| : |||
Db      402 HDAKLAGYD 410
```

```
RESULT 28
US-10-667-295-81
; Sequence 81, Application US/10667295
; Publication No. US20050257293A1
; GENERAL INFORMATION:
; APPLICANT: Masclia, Peter
; TITLE OF INVENTION: BIOLOGICAL CONTAINMENT SYSTEM
; FILE REFERENCE: 11696-047001
; CURRENT APPLICATION NUMBER: US/10/667,295
; CURRENT FILING DATE: 2003-09-17
; PRIOR APPLICATION NUMBER: US 60/411,823
; PRIOR FILING DATE: 2002-09-17
; NUMBER OF SEQ ID NOS: 263
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 81
; LENGTH: 534
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)...(534)
; OTHER INFORMATION: Ceres Seq. ID no. 12558790
US-10-667-295-81
```

```
Query Match      57.3%; Score 27.5; DB 6; Length 534;
Best Local Similarity 66.7%; Pred. No. 1.3e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 1; Gaps 1;
```

```
OY      1 HDAP1-GYD 8
        ||| : |||
Db      410 HDAKLAGYD 418
```

```
RESULT 29
US-10-467-657-412
; Sequence 412, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SPA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqMan99, version 1.04
; SEQ ID NO 412
; LENGTH: 54
```

TYPE: PRT
ORGANISM: Neisseria gonorrhoeae
US-10-467-657-412

Query Match 56.2%; Score 27; DB 6; Length 54;
Best Local Similarity 66.7%; Pred. No. 14;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 HDAPIG 6
Db 2 HDSBAG 7

RESULT 30
US-10-467-657-3158

; Sequence 3158, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SPA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; PRIOR FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 3158
; LENGTH: 92
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-3158

Query Match 56.2%; Score 27; DB 6; Length 92;
Best Local Similarity 66.7%; Pred. No. 24;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 HDAPIG 6
Db 46 HSAPIG 51

RESULT 31
US-10-467-657-2310

; Sequence 2310, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SPA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; PRIOR FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 2310
; LENGTH: 405
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-2310

Query Match 56.2%; Score 27; DB 6; Length 405;
Best Local Similarity 83.3%; Pred. No. 1.2e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 APGYD 8
Db 103 APGYD 108

RESULT 32
US-10-467-657-1858

; Sequence 1858, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SPA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; PRIOR FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 1858
; LENGTH: 413
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-1858

Query Match 56.2%; Score 27; DB 6; Length 413;
Best Local Similarity 66.7%; Pred. No. 1.2e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 HDAPIG 6
Db 155 HHAAPVG 160

RESULT 33
US-10-467-657-4570

; Sequence 4570, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SPA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; PRIOR FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 4570
; LENGTH: 435
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-4570

Query Match 56.2%; Score 27; DB 6; Length 435;
Best Local Similarity 57.1%; Pred. No. 1.3e+02;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 HDAPIG 7
Db 258 HDAVIGF 264

RESULT 34

US-10-793-626-1200
; Sequence 1200, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
; APPLICANT: KIMBERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PUS480US
; CURRENT APPLICATION NUMBER: US/10/793,626
; CURRENT FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1200
; LENGTH: 443
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-10-793-626-1200

Query Match 56.2%; Score 27; DB 6; Length 443;
Best Local Similarity 57.1%; Pred. No. 1.3e+02;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 DAPIGYD 8
|:|
|:|
Db 49 DLPVDYD 55

RESULT 35
US-10-467-657-6146
; Sequence 6146, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SPA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqMan99, version 1.04
; SEQ ID NO 6146
; LENGTH: 528
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-6146

Query Match 56.2%; Score 27; DB 6; Length 528;
Best Local Similarity 66.7%; Pred. No. 1.6e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 DAPIGYD 7
|:|
|:|
Db 353 DPLGYD 358

RESULT 36
US-10-467-657-468
; Sequence 468, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SPA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega

APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqMan99, version 1.04
; SEQ ID NO 468
; LENGTH: 544
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-468

Query Match 56.2%; Score 27; DB 6; Length 544;
Best Local Similarity 50.0%; Pred. No. 1.6e+02;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 HDAPGYD 8
|:|
|:|
Db 127 HEGMAGYD 134

RESULT 37
US-11-082-389-436
; Sequence 436, Application US/11082389
; Publication No. US20050244935A1
; GENERAL INFORMATION:
; APPLICANT: Pompeius, Markus
; APPLICANT: Kroeger, Burkhard
; APPLICANT: Schroder, Hartwig
; APPLICANT: Zelder, Oskar
; APPLICANT: Haberhauser, Gregor
; TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING PROTEINS
; TITLE OF INVENTION: INVOLVED IN MEMBRANE SYNTHESIS AND MEMBRANE
; TITLE OF INVENTION: TRANSPORT
; FILE REFERENCE: BG1-131CPCN
; CURRENT APPLICATION NUMBER: US/11/082,389
; CURRENT FILING DATE: 2005-03-16
; PRIOR APPLICATION NUMBER: US 09/603024
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: US 60/141031
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: US 60/143262
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: US 60/151281
; PRIOR FILING DATE: 1999-08-27
; PRIOR APPLICATION NUMBER: DE 19930487.4
; PRIOR FILING DATE: 1999-07-01
; PRIOR APPLICATION NUMBER: DE 19930489.0
; PRIOR FILING DATE: 1999-07-01
; PRIOR APPLICATION NUMBER: DE 19931549.3
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931550.7
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19932134.5
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19941379.7
; PRIOR FILING DATE: 1999-08-31
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 446
; SEQ ID NO 436
; LENGTH: 611
; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-11-082-389-436

Query Match 56.2%; Score 27; DB 7; Length 611;
Best Local Similarity 57.1%; Pred. No. 1.9e+02;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 DAPIGYD 8

Db 148 DGPVEYD 154

RESULT 38

US-10-467-657-2008
; Sequence 2008, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SPA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 2008
; LENGTH: 680
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-2008

Query Match 56.2%; Score 27; DB 6; Length 680;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 DAPIG 6
Db 50 DAPIG 54

RESULT 39

US-10-467-657-8694
; Sequence 8694, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SPA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 8694
; LENGTH: 756
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-8694

Query Match 56.2%; Score 27; DB 6; Length 756;
Best Local Similarity 66.7%; Pred. No. 2.3e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 3 APIGYD 8
Db 541 SPIGPD 546

RESULT 40
US-10-467-657-78
; Sequence 78, Application US/10467657

; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SPA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 78
; LENGTH: 872
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-78

Query Match 56.2%; Score 27; DB 6; Length 872;
Best Local Similarity 62.5%; Pred. No. 2.7e+02;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 HDAPIGYD 8
Db 674 NDPIGID 681

Search completed: December 3, 2005, 23:45:54
Job time : 12 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 3, 2005, 23:23:38 / Search time 37 Seconds
(without alignments)
20.804 Million cell updates/sec

Title: US-10-807-553-2
Perfect score: 48
Sequence: 1 HDAPIGYD 8

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database :
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	48	100.0	736	1	KIRBCE
2	48	100.0	737	1	KIRSCB
3	48	100.0	737	1	KIRSCB
4	48	100.0	737	1	KIRSCB
5	39	81.2	652	1	T39409
6	39	81.2	869	1	UC4858
7	38	79.2	682	1	A39666
8	38	79.2	683	1	A23690
9	38	79.2	683	1	S29478
10	38	79.2	1025	2	T10259
11	37	77.1	2203	2	T42742
12	35	72.9	180	2	T47414
13	35	72.9	199	2	AC3241
14	35	72.9	371	2	T26389
15	35	72.9	400	2	T41569
16	35	72.9	457	2	UC5422
17	35	72.9	468	2	S45145
18	35	72.9	471	1	S14733
19	35	72.9	471	2	H84363
20	35	72.9	699	2	A83838
21	35	72.9	1023	2	A47296
22	34.5	71.9	553	2	T06499
23	34	70.8	205	2	D71918
24	34	70.8	290	2	S36706
25	34	70.8	304	2	T42554
26	34	70.8	312	2	T50960
27	34	70.8	326	2	T29810
28	34	70.8	326	2	JS0169
29	34	70.8	392	2	AB2474

30	34	70.8	411	2	A96985	uncharacterized co
31	34	70.8	423	2	B64157	hypothetical prote
32	34	70.8	432	2	B65190	potassium uptake p
33	34	70.8	483	2	A91226	potassium uptake p
34	34	70.8	483	2	G86072	tyk system potassi
35	34	70.8	483	2	AB0458	methionine-cRNA 11
36	34	70.8	547	2	D84942	methionine-cRNA 11
37	34	70.8	550	2	H81718	methionine-cRNA 11
38	34	70.8	550	2	C71567	methionine-cRNA 11
39	34	70.8	551	2	H72117	methionine-cRNA 11
40	34	70.8	551	2	C86506	methionine-cRNA 11
41	34	70.8	551	2	H81552	methionine-cRNA 11
42	34	70.8	658	2	D69431	methionine-cRNA 11
43	34	70.8	675	2	AF0185	methionine-cRNA 11
44	34	70.8	677	1	SYECMT	methionine-cRNA 11
45	34	70.8	677	2	AH0776	methionine-cRNA 11
46	34	70.8	677	2	C83210	methionine-cRNA 11
47	34	70.8	677	2	C85839	methionine-cRNA 11
48	34	70.8	677	2	H90993	methionine-cRNA 11
49	34	70.8	682	2	T64113	methionine-cRNA 11
50	34	70.8	702	2	C82792	methionine-cRNA 11
51	34	70.8	731	2	D82249	methionine-cRNA 11
52	34	70.8	734	2	B70173	methionine-cRNA 11
53	34	70.8	797	2	T05247	methionine-cRNA 11
54	34	70.8	917	2	T22898	hypothetical prote
55	34	70.8	989	2	T02568	hypothetical prote
56	34	70.8	1131	2	A23944	chitin synthase (E
57	34	68.8	164	2	B81942	probable 2-amino-4
58	34	68.8	164	2	H81162	2-amino-4-hydroxy
59	33	68.8	210	2	AC0667	ribulose-phosphate
60	33	68.8	246	2	G88366	protein C04H5.4 [1
61	33	68.8	483	2	G81745	conserved hypochet
62	33	68.8	483	2	AE0914	trk system potassi
63	33	68.8	505	2	T18933	hypothetical prote
64	33	68.8	509	2	G96552	unknown protein, 6
65	33	68.8	512	2	F83761	fructarase hydrata
66	33	68.8	513	2	T37180	probable membrane
67	33	68.8	530	2	T18932	hypothetical prote
68	33	68.8	554	2	G82272	DNA repair protein
69	33	68.8	685	2	A81246	methionyl-cRNA syn
70	33	68.8	685	2	G82022	methionine-cRNA 11
71	33	68.8	811	2	E71281	methionine-cRNA 11
72	33	68.8	1955	2	T41170	probable 1,3-beta-
73	33	66.7	50	2	H97655	hypothetical prote
74	32	66.7	139	2	B70925	hypothetical prote
75	32	66.7	319	2	S35928	6-phosphofructokin
76	32	66.7	322	2	T40718	probable transmemb
77	32	66.7	324	2	A37767	stress-inducible p
78	32	66.7	384	2	H84405	hypothetical prote
79	32	66.7	418	2	T34606	probable fumarylac
80	32	66.7	463	2	AP0469	probable permease
81	32	66.7	472	2	G01872	benzylum-binding p
82	32	66.7	572	2	S72249	trithorax protein
83	32	66.7	581	2	S62505	probable alpha-amy
84	32	66.7	588	2	A26158	decapentaplegic pr
85	32	66.7	598	2	T51368	gamma-aminobutyric
86	32	66.7	598	2	T25207	hypothetical prote
87	32	66.7	599	2	D83764	chitinase BHO916 [
88	32	66.7	612	2	E87790	aminopeptidase hom
89	32	66.7	795	2	AD0296	phenylalanine-cRNA
90	32	66.7	1174	1	HJBYDH	helicase (EC 3.6.1
91	32	66.7	1231	2	AF2220	hypothetical prote
92	32	66.7	1737	2	T00209	MGF8 protein - hu
93	32	65.6	357	2	B47411	ADP-ribosylarginine
94	31.5	65.6	362	2	A47411	ADP-ribosylarginine
95	31.5	65.6	362	2	A38135	ADP-ribosylarginine
96	31	64.6	99	2	G95971	hypothetical expor
97	31	64.6	145	2	AD2855	hypothetical prote
98	31	64.6	192	2	AH3643	cytochrome b561 [i
99	31	64.6	199	2	AB3172	conserved hypochet
100	31	64.6	205	2	T43554	ubiquitin fusion d

ALIGNMENTS

RESULT 1

KIRRC

C/Species: *Oryctolagus cuniculus* (domestic rabbit)
C/Date: 30-Sep-1992 #sequence_revision 30-Sep-1992 #text_change 05-Oct-2004
C/Accession: A29880R:Ohno, S.; Akita, Y.; Kono, Y.; Imajoh, S.; Suzuki, K.
Cell 53, 731-741, 1988A>Title: A novel photol ester receptor/protein kinase, nPKC, distantly related to the p
A/Reference number: A29880; MUID:88223367; PMID:3370672
A/Molecule type: mRNAA/Residues: 1-736 <OHN>
A/Cross-references: UNIPARC:UPI0000172502; GB:M20014C/Function: A:Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonin
A>Note: activity is calcium-independent, phospholipid-dependent, and activated by diacyl
C/Superfamily: protein kinase C, delta/epsilon/eta/theta types; protein kinase C zinc-bl
C/Keywords: ATP; autophosphorylation; duplication; phorbol ester binding; phospholipid bF:156-161/Region: pseudophosphorylation motif
F:1170-220/Domain: protein kinase C zinc-binding repeat homology <K21>
F:1243-292/Domain: protein kinase C zinc-binding repeat homology <K22>
F:406-667/Domain: protein kinase homology <KIN>
F:414-422/Region: protein kinase ATP-binding motifF:1170,201,204,220/Binding site: zinc (His, Cys, Cys, Cys) #status predicted
F:183,186,209,212/Binding site: zinc (Cys, Cys, His, Cys) #status predicted
F:243,223,276,292/Binding site: zinc (His, Cys, Cys, Cys) #status predicted
F:256,259,281,284/Binding site: zinc (Cys, Cys, His, Cys) #status predicted
F:435,455,531,533/Active site: Lys, Glu, Asp, Lys #status predictedF:702,709/Binding site: phosphate (Thr) (covalent) (by autophosphorylation) #status pred
Query Match 100.0%; Score 48; DB 1; Length 736;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;Qy 1 HDAPIGYD 8
Db 85 HDAPIGYD 92

RESULT 2

KIMSCB

C/Species: *Mus musculus* (house mouse)
C/Date: 30-Sep-1992 #sequence_revision 30-Sep-1992 #text_change 05-Oct-2004
C/Accession: S02270R:Schnap, D.; Parker, P.J.; Bristol, A.; Kriz, R.; Knopf, J.
FEBS Lett. 243, 351-357, 1989A>Title: Unique substrate specificity and regulatory properties of PKC-epsilon: a ratio
A/Reference number: S02270; MUID:89137541; PMID:2917656
A/Accession: S02270A/Status: nucleic acid sequence not shown; not compared with conceptual translation
A/Molecule type: mRNA
A/Residues: 1-737 <SCH>
A/Cross-references: UNIPROT:P16054; UNIPARC:UPI0000029722C/Function: A:Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonin
A>Note: activity is calcium-independent, phospholipid-dependent, and activated by diacyl
C/Superfamily: protein kinase C, delta/epsilon/eta/theta types; protein kinase C zinc-bl
C/Keywords: ATP; autophosphorylation; duplication; phorbol ester binding; phospholipid bF:156-161/Region: pseudophosphorylation motif
F:1170-220/Domain: protein kinase C zinc-binding repeat homology <K21>
F:1243-292/Domain: protein kinase C zinc-binding repeat homology <K22>
F:406-667/Domain: protein kinase homology <KIN>
F:414-422/Region: protein kinase ATP-binding motifF:1170,201,204,220/Binding site: zinc (His, Cys, Cys, Cys) #status predicted
F:183,186,209,212/Binding site: zinc (Cys, Cys, His, Cys) #status predicted
F:243,223,276,292/Binding site: zinc (His, Cys, Cys, Cys) #status predicted
F:256,259,281,284/Binding site: zinc (Cys, Cys, His, Cys) #status predicted

F:437,456,532/Active site: Lys, Glu, Asp, Lys #status predicted

F:703,710/Binding site: phosphate (Thr) (covalent) (by autophosphorylation) #status predi

Query Match 100.0%; Score 48; DB 1; Length 737;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;Qy 1 HDAPIGYD 8
Db 85 HDAPIGYD 92

RESULT 3

KIRRC

C/Species: *Rattus norvegicus* (Norway rat)
C/Date: 30-Sep-1992 #sequence_revision 30-Sep-1992 #text_change 05-Oct-2004
C/Accession: B28163; B26408; S00216R:Ohno, Y.; Fujii, T.; Ogita, K.; Kikkawa, U.; Igarehnl, K.; Nishizuka, Y.
J. Biol. Chem. 263, 6927-6932, 1988A>Title: The structure, expression, and properties of additional members of the protein y
A/Reference number: A92717; MUID:88198270; PMID:2834397
A/Accession: B28163A/Molecule type: DNA
A/Residues: 1-737 <ONQ>A/Cross-references: UNIPROT:P09216; UNIPARC:UPI000012056D; GB:M18331; NID:G206182; PIDN:1;
R:Housey, G.M.; O'Brian, C.A.; Johnson, M.D.; Kirschmeier, P.; Weinstein, I.B.
Proc. Natl. Acad. Sci. U.S.A. 84, 1065-1069, 1987A>Title: Isolation of cDNA clones encoding protein kinase C: evidence for a protein kina
A/Reference number: A94145; MUID:87147193; PMID:3469647
A/Accession: B26408A/Molecule type: mRNA
A/Residues: 397-447; GQGRGLHDDREDFSGAGET, 467, USNFTLLILPQGPPLURQ, 487-545, C, 547-636
A/Cross-references: UNIPARC:UPI000006662B; GB:M15523; NID:G206192; PIDN:AAA41977.1; PIDN:
C/Comment: Protein kinase C epsilon and epsilon' appear to be encoded by the same gene aC/Function: A:Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonin
A>Note: activity is calcium-independent, phospholipid-dependent, and activated by diacyl
C/Superfamily: protein kinase C, delta/epsilon/eta/theta types; protein kinase C zinc-bl
C/Keywords: alternative splicing; ATP; autophosphorylation; duplication; phorbol ester bF:156-161/Region: pseudophosphorylation motif
F:1170-220/Domain: protein kinase C zinc-binding repeat homology <K21>
F:1243-292/Domain: protein kinase C zinc-binding repeat homology <K22>
F:406-667/Domain: protein kinase homology <KIN>
F:414-422/Region: protein kinase ATP-binding motifF:1170,201,204,220/Binding site: zinc (His, Cys, Cys, Cys) #status predicted
F:183,186,209,212/Binding site: zinc (Cys, Cys, His, Cys) #status predicted
F:243,223,276,292/Binding site: zinc (His, Cys, Cys, Cys) #status predicted
F:256,259,281,284/Binding site: zinc (Cys, Cys, His, Cys) #status predictedF:437,456,532/Active site: Lys, Glu, Asp, Lys #status predicted
F:703,710/Binding site: phosphate (Thr) (covalent) (by autophosphorylation) #status pred
Query Match 100.0%; Score 48; DB 1; Length 737;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;Qy 1 HDAPIGYD 8
Db 85 HDAPIGYD 92

RESULT 4

KIMSCB

C/Species: *Homo sapiens* (man)
C/Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 05-Oct-2004
C/Accession: S28942R:Baetza, P.; Strickland, M.B.; Holmes, W.; Loomis, C.R.; Ballas, L.M.; Burns, D.J.
Biochim. Biophys. Acta 1132, 154-160, 1992A>Title: Sequence and expression of human protein kinase C-epsilon.
A/Reference number: S28942; MUID:93003318; PMID:1382605
A/Accession: S28942

A/Status: preliminary

A:Molecule type: mRNA
A:Residues: 1-737 <BAS>
A:Cross-references: UNIPROT:O02156; UNIPARC:UPI000012DF6B; EMBL:X65293; NID:g315494; PIDN
C:Comment: This is a calcium-independent, phospholipid-dependent, serine- and threonine-
of inositol phospholipids. This protein is a receptor for tumor-promoting phorbol ester
C:Genetics:
A:Gene: GDB:PRKCE
A:Cross-references: GDB:128039; OMIM:176975
A:Map position: 3pter-3qter
C:Function:
A:Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonin
A:Note: activity is calcium-independent, phospholipid-dependent, and activated by diacyl
C:Superfamily: protein kinase C, delta/epsilon/eta/theta types; protein kinase C zinc-bi
C:Keywords: ATP; duplication; phorbol ester binding; phospholipid binding; phosphotransf
F:156-161/Region: pseudophosphorylation motif
F:170-220/Domain: protein kinase C zinc-binding repeat homology <KZ1>
F:243-252/Domain: protein kinase C zinc-binding repeat homology <KZ2>
F:406-668/Domain: protein kinase homology <KIN>
F:414-422/Region: protein kinase ATP-binding motif
F:170,201,204,220/Binding site: zinc (His, Cys, Cys, His, Cys) #status predicted
F:183,186,209,212/Binding site: zinc (Cys, Cys, His, Cys) #status predicted
F:243,273,276,292/Binding site: zinc (His, Cys, Cys, Cys) #status predicted
F:256,259,281,284/Binding site: zinc (Cys, Cys, His, Cys) #status predicted
F:437,456,532,534/Active site: Lys, Glu, Asp, Lys #status predicted

Query Match 100.0%; Score 48; DB 1; Length 737;
Best Local Similarity 100.0%; Pred. No. 0.14; Mismatches 0; Gaps 0;
Matches 8; Conservative 0; Indels 0; Gaps 0;

Qy 1 HDAPIGYD 8
Db 85 HDAPIGYD 92

RESULT 5
T39409
hypothetical protein SPBC13G1.08c - fission yeast (Schizosaccharomyces pombe)
C:Species: Schizosaccharomyces pombe
C>Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C:Accession: T39409
R:Lyne, M.; Wood, V.; Rajandream, M.A.; Barrell, B.G.; Badcock, K.; Churcher, C.M.
submitted to the EMBL Data Library, April 1998
A:Reference number: Z21852
A:Accession: T39409
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-652 <LYN>
A:Cross-references: UNIPROT:O60070; UNIPARC:UPI000006ADAC; EMBL:AL022600; PIDN:CAA18661.
C:Genetics:
A:Experimental source: strain 972h-; cosmid c13G1
A:Gene: SPDB:SPBC13G1.08c
A:Map position: 2

Query Match 81.2%; Score 39; DB 2; Length 652;
Best Local Similarity 85.7%; Pred. No. 7.9; Mismatches 0; Gaps 0;
Matches 6; Conservative 1; Indels 0; Gaps 0;

Qy 2 DAPIGYD 8
Db 419 DAPIGYD 425

RESULT 6
JC4858
VLDL receptor precursor - African clawed frog
N:Alternate names: very low density lipoprotein receptor; vitellogenin receptor
C:Species: Xenopus laevis (African clawed frog)
C>Date: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 09-Jul-2004
C:Accession: JC4858
R:Okabayashi, K.; Shoji, H.; Nakamura, T.; Hashimoto, O.; Asaahina, M.; Sugino, H.
Biochem. Biophys. Res. Commun. 224, 406-413, 1996
A:Title: cDNA cloning and expression of the Xenopus laevis vitellogenin receptor.
A:Reference number: JC4858; MUID:96295501; PMID:8702402

A:Accession: JC4858
A:Molecule type: mRNA
A:Residues: 1-869 <OKA>
A:Cross-references: UNIPROT:O42126; UNIPARC:UPI00000FBB42; GB:AB00606; NID:g2366772; PIDN
C:Comment: This receptor mediates incorporation of vitellogenin into oocytes.
C:Superfamily: LDL receptor; EGF homology; LDL receptor ligand-binding repeat homology; I
C:Keywords: duplication; fatty acid metabolism; glycoprotein; receptor; transmembrane p
F:1-26/Domain: signal sequence #status predicted <SIG>
F:27-869/Product: VLDL receptor #status predicted <MAT>
F:27-793/Domain: extracellular #status predicted <EXT>
F:32-66/Domain: LDL receptor ligand-binding repeat homology <LDL1>
F:71-107/Domain: LDL receptor ligand-binding repeat homology <LDL2>
F:112-148/Domain: LDL receptor ligand-binding repeat homology <LDL3>
F:153-187/Domain: LDL receptor ligand-binding repeat homology <LDL4>
F:192-228/Domain: LDL receptor ligand-binding repeat homology <LDL5>
F:238-272/Domain: LDL receptor ligand-binding repeat homology <LDL6>
F:277-311/Domain: LDL receptor ligand-binding repeat homology <LDL7>
F:317-354/Domain: LDL receptor ligand-binding repeat homology <LDL8>
F:359-393/Domain: EGF homology <EG1>
F:399-433/Domain: EGF homology <EG2>
F:440-479/Domain: LDL receptor WYTD-containing repeat homology <YW1>
F:480-525/Domain: LDL receptor WYTD-containing repeat homology <YW2>
F:526-568/Domain: LDL receptor WYTD-containing repeat homology <YW3>
F:569-612/Domain: LDL receptor WYTD-containing repeat homology <YW4>
F:613-655/Domain: LDL receptor WYTD-containing repeat homology <YW5>
F:656-698/Domain: LDL receptor WYTD-containing repeat homology <YW6>
F:707-749/Domain: EGF homology <EG3>
F:794-815/Domain: transmembrane #status predicted <TM>
F:816-869/Domain: intracellular #status predicted <CY>
F:830-834/Region: coated-pit mediated internalization signal
F:150,201,777,786/Binding site: carbohydrate (asn) (covalent) #status predicted
F:359-370,366-379,381-393,399-409,405-418,420-433,707-720,716-725,737-749/Dissulfide bond

Query Match 81.2%; Score 39; DB 1; Length 869;
Best Local Similarity 75.0%; Pred. No. 11; Mismatches 1; Indels 0; Gaps 0;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 HDAPIGYD 8
Db 371 HDAPIGYD 378

RESULT 7
A39666
protein kinase C (EC 2.7.1.-) eta - human
N:Alternate names: protein kinase C PKC-L
C:Species: Homo sapiens (man)
C>Date: 08-Nov-1991 #sequence_revision 11-Apr-1997 #text_change 05-Oct-2004
C:Accession: A39666; A42131; S65018
R:Bacher, N.; Zisman, Y.; Berent, E.; Lavneh, E.
Mol. Cell. Biol. 11, 126-133, 1991
A:Title: Isolation and characterization of PKC-L, a new member of the protein kinase C-re
A:Reference number: A39666; MUID:91094824; PMID:1986216
A:Accession: A39666
A:Molecule type: mRNA
A:Residues: 1-276; 'YNBCAY', 'SMSSSRG', 297-296, 'MRWV', 301, 'PRP', 'GRD', 309-682 <BA2>
A:Cross-references: UNIPROT:P24723; UNIPARC:UPI0000172503; GB:M55284; NID:g189988; PIDN:
C:Note: the cross-reference is to the corrected sequence
R:Bacher, N.; Zisman, Y.; Berent, E.; Lavneh, E.
Mol. Cell. Biol. 12, 1404, 1992
A:Title: Isolation and characterization of PKC-L, a new member of the protein kinase C-re
A:Reference number: A42131; MUID:92168874; PMID:1545821
A:Contents: erratum
A:Accession: A42131
A:Molecule type: mRNA
A:Residues: 277-308 <BA3>
A:Cross-references: UNIPARC:UPI0000172504; GB:M55284
A:Note: this report is a revision to reference A39666
R:Palmer, R.H.; Ridden, J.; Parker, P.J.
FEBS Lett. 356, 5-8, 1994
A:Title: Identification of multiple, novel, protein kinase C-related gene products.
A:Reference number: S51020; MUID:95080426; PMID:7988719
A:Accession: S65018

A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 437-470, 'E', 472-538 <PAL>
A;Cross-references: UNIPARC:UPI000016B45B; EMBL:S74620; NID:G786485; PIDN:AA832724.1; P2
C;Genetics:
A;Gene: GDB:PRKCH; PKC- ζ , PRKCL
A;Cross-references: GDB:129009
A;Map position: 19q13.4-19q13.4
C;Function:
A;Description: catalyzes protein phosphorylation at Ser or Thr residues
A;Note: activity is calcium-independent, phospholipid-dependent, and activated by diacyl
C;Superfamily: protein kinase C, delta/epsilon/eta/theta types; protein kinase C zinc-bi
C;Keywords: ATP; autophosphorylation; duplication; phorbol ester binding; phospholipid b
F;171-221/Domain: pseudophosphorylation motif
F;171-221/Domain: protein kinase C zinc-binding repeat homology <K21>
F;245-294/Domain: protein kinase C zinc-binding repeat homology <K22>
F;353-613/Domain: protein kinase homology <KIN>
F;361-369/Region: protein kinase ATP-binding motif
F;171,202,205,221/Binding site: zinc (His, Cys, Cys, Cys) #status predicted
F;184,187,210,213/Binding site: zinc (Cys, Cys, His, Cys) #status predicted
F;245,275,278,294/Binding site: zinc (His, Cys, Cys, Cys) #status predicted
F;259,261,283,286/Binding site: zinc (Cys, Cys, His, Cys) #status predicted
F;384,403,478,480/Active site: Lys, Glu, Asp, Lys #status predicted

Query Match 79.2%; Score 38; DB 1; Length 682;
Best Local Similarity 62.5%; Pred. No. 13;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 HDAPIGYD 8
Db 88 HETPLGYD 95

RESULT 8
A23690
Protein kinase (BC 2.7.1.37) eta - mouse
C;Species: Mus musculus (house mouse)
C;Date: 04-Oct-1991 #sequence_revision 04-Oct-1991 #text_change 05-Oct-2004
C;Accession: A23690
R;Osada, S.; Mizuno, K.; Saigo, T.C.; Akita, Y.; Suzuki, K.; Kuroki, T.; Ohno, S.
J. Biol. Chem. 265, 22434-22440, 1990
A;Title: A phorbol ester receptor/protein kinase, nPKC-eta, a new member of the protein
A;Reference number: A23690; MUID:91093089; PMID:2265135
A;Accession: A23690
A;Molecule type: mRNA
A;Residues: 1-683 <OSA>
A;Cross-references: UNIPROT:223298; UNIPARC:UPI0000029755; GB:D90242; GB:J05703; NID:922
C;Function:
A;Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonine
A;Note: activity is calcium-independent, phospholipid-dependent, and activated by diacyl
C;Superfamily: protein kinase C, delta/epsilon/eta/theta types; protein kinase C zinc-bi
C;Keywords: ATP; autophosphorylation; duplication; phorbol ester binding; phospholipid b
F;158-163/Region: pseudophosphorylation motif
F;172-222/Domain: protein kinase C zinc-binding repeat homology <K21>
F;245-295/Domain: protein kinase C zinc-binding repeat homology <K22>
F;353-614/Domain: protein kinase homology <KIN>
F;361-369/Region: protein kinase ATP-binding motif
F;171,203,206,222/Binding site: zinc (His, Cys, Cys, Cys) #status predicted
F;185,188,211,214/Binding site: zinc (Cys, Cys, His, Cys) #status predicted
F;246,276,279,295/Binding site: zinc (His, Cys, Cys, Cys) #status predicted
F;259,261,284,287/Binding site: zinc (Cys, Cys, His, Cys) #status predicted
F;384,403,479,481/Active site: Lys, Glu, Asp, Lys #status predicted

Query Match 79.2%; Score 38; DB 1; Length 683;
Best Local Similarity 62.5%; Pred. No. 13;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 HDAPIGYD 8
Db 88 HETPLGYD 95

RESULT 9

S29478
Protein kinase C (BC 2.7.1.-) eta - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 05-Oct-2004
C;Accession: I60246; S29478
R;Decker, L.V.; Parker, P.J.; McIntyre, P.
FEBS Lett. 312, 195-199, 1992
A;Title: Biochemical properties of rat protein kinase C-eta expressed in COS cells.
A;Reference number: I60246; MUID:93050193; PMID:11426252
A;Accession: I60246
A;Status: translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-683 <RES>
A;Cross-references: UNIPROT:Q64617; UNIPARC:UPI000012PF72; EMBL:X68400; NID:956915; PIDN:
C;Function:
A;Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonine
A;Note: activity is calcium-independent, phospholipid-dependent, and activated by diacyl
C;Superfamily: protein kinase C, delta/epsilon/eta/theta types; protein kinase C zinc-bi
C;Keywords: ATP; autophosphorylation; duplication; phorbol ester binding; phospholipid bi
F;158-163/Region: pseudophosphorylation motif
F;172-222/Domain: protein kinase C zinc-binding repeat homology <K21>
F;246-295/Domain: protein kinase C zinc-binding repeat homology <K22>
F;353-614/Domain: protein kinase homology <KIN>
F;361-369/Region: protein kinase ATP-binding motif
F;172,203,206,222/Binding site: zinc (His, Cys, Cys, Cys) #status predicted
F;185,188,211,214/Binding site: zinc (Cys, Cys, His, Cys) #status predicted
F;246,276,279,295/Binding site: zinc (His, Cys, Cys, Cys) #status predicted
F;259,262,284,287/Binding site: zinc (Cys, Cys, His, Cys) #status predicted
F;384,403,479,481/Active site: Lys, Glu, Asp, Lys #status predicted

Query Match 79.2%; Score 38; DB 1; Length 683;
Best Local Similarity 62.5%; Pred. No. 13;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 HDAPIGYD 8
Db 88 HETPLGYD 95

RESULT 10
T10259
RNA-directed DNA polymerase (BC 2.7.7.49) - pteromalid wasp (Nasonia vitripennis) retroc
C;Species: Nasonia vitripennis
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004
C;Accession: T10259; I44490
R;Burke, W.D.; Malik, H.S.; Latche III, W.C.; Blackbush, T.H.
Nature 392, 141-142, 1998
A;Title: Are retrotransposons long-term hitchhikers?
A;Reference number: Z17001; MUID:98175715; PMID:9515960
A;Accession: T10259
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-1025 <BUR>
A;Cross-references: UNIPROT:Q03278; UNIPARC:UPI000031D75; EMBL:L00950; NID:93559783; PI
R;Burke, W.D.; Blackbush, D.G.; Xiong, Y.; Jakubczak, J.; Blackbush, T.H.
Mol. Biol. Evol. 10, 163-185, 1993
A;Title: Sequence relationship of retrotransposable elements R1 and R2 within and between
A;Reference number: A44490; MUID:93196484; PMID:8383793
A;Contents: retrotransposable element R2
A;Accession: I44490
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: DNA
A;Residues: 314-956, 'Q', 'A', '971', 'AA' <BU2>
A;Cross-references: UNIPARC:UPI000017BF02
A;Note: sequence extracted from NCBI backbone (NCBI:P127243)
C;Genetics:
A;Mobile element: retrotransposon R2
C;Keywords: nucleotidyltransferase

Query Match 79.2%; Score 38; DB 2; Length 1025;
Best Local Similarity 85.7%; Pred. No. 20;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 HDAPIGY 7
|||
Db 709 HDTPIGY 715

RESULT 11

T42742
voltage-dependent calcium channel alpha 1 chain, isoform CACNA4 - rat
C:Species: Rattus norvegicus (Norway rat)
C>Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 21-Jul-2000
C:Accession: T42742
R:Inara, Y.; Yamada, Y.; Fujii, Y.; Gonori, T.; Yano, H.; Yaeuda, K.; Inagaki, N.; Seino
Mol. Endocrinol. 9, 121-130, 1995
A:Title: Molecular diversity and functional characterization of voltage-dependent calcium
A:Reference number: 222258, MUID:95280950, PMID:7760845
A:Accession: T42742
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-2203 <IHA>
A:Cross-references: UNIPARC:UPI0000127274; EMBL:D38101; NID:9736711; PIDN:BAA07282.1; PI
A:Experimental source: Insulinoma RINm5F complementary DNA library
C:Superfamily: voltage-dependent calcium channel protein alpha-1 chain
C:Keywords: calcium channel

Query Match 77.1%; Score 37; DB 2; Length 2203;
Best Local Similarity 85.7%; Pred. No. 74;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 DAPIGYD 8
|||
Db 1937 DSPIGYD 1943

RESULT 12

T47414
hypothetical protein T28A8.70 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 09-Jul-2004
C:Accession: T47414
R:Purnelle, B.; Boutty, M.; Goffeau, A.; Mewes, H.W.; Rudd, S.; Lemcke, K.; Mayer, K.F.X
submitted to the Protein Sequence Database, March 2000
A:Reference number: 224466
A:Accession: T47414
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-180 <PUR>
A:Cross-references: UNIPROT:Q9LZG9; UNIPARC:UPI0000044221; EMBL:AL162691
A:Experimental source: cultivar Columbia; BAC clone T28A8
C:Genetics:
A:Map position: 3
A:Intons: 21/2; 32/2; 91/3; 105/3
A>Note: T28A8.70

Query Match 72.9%; Score 35; DB 2; Length 180;
Best Local Similarity 75.0%; Pred. No. 13;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 HDAPIGYD 8
|||
Db 38 HDIPIGYD 45

RESULT 13

AC3241
conserved hypothetical protein Atu6109 [imported] - Agrobacterium tumefaciens (strain C5
C:Species: Agrobacterium tumefaciens
C>Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 09-Jul-2004
C:Accession: AC3241
R:Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, L
erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kutayavin, T.; Levy, R.; Li, M.; McClell
; Kap, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A:Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,

ster, E.W.
A:Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A:Reference number: AB2577; MUID:21608550; PMID:11743193

A:Accession: AC3241
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-199 <KUR>
A:Cross-references: UNIPROT:Q8U626; UNIPARC:UPI000002799; GB:AE008690; PIDN:AA146345.1;
A:Experimental source: strain C58 (Dupont)
C:Genetics:
A:Gene: Atu6109
A:Genome: plasmid

Query Match 72.9%; Score 35; DB 2; Length 199;
Best Local Similarity 71.4%; Pred. No. 14;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 DAPIGYD 8
|||
Db 127 DGPVGYD 133

RESULT 14

T26389
hypothetical protein Y105CSB.m - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T26389
R:McMurray, A.
submitted to the EMBL Data Library, September 1999
A:Reference number: 220208
A:Accession: T26389
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-371 <WIL>
A:Cross-references: UNIPROT:Q9NAMS; UNIPARC:UPI0000061216; EMBL:AL110479; NID:e1542153; I
A:Experimental source: clone Y105CSB
C:Genetics:
A:Gene: CBSP.Y105CSB.m
A:Intons: 24/1; 56/1; 101/3; 138/2; 219/3; 290/3; 332/2

Query Match 72.9%; Score 35; DB 2; Length 371;
Best Local Similarity 85.7%; Pred. No. 28;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 DAPIGYD 8
|||
Db 59 DLPIGYD 65

RESULT 15

T41569
hypothetical protein SPCC736.12c - fission yeast (Schizosaccharomyces pombe)
C:Species: Schizosaccharomyces pombe
C>Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C:Accession: T41569
R:Wood, V.; Rajandream, M.A.; Barrell, B.G.; Murphy, L.; Harris, D.
submitted to the EMBL Data Library, May 1998
A:Reference number: 221991
A:Accession: T41569
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-400 <MO>
A:Cross-references: UNIPROT:O74950; UNIPARC:UPI0000178200; EMBL:AL023705; PIDN:CAA19276.1
A:Experimental source: strain 972h-; cosmid c736
C:Genetics:
A:Gene: SPDB:SPCC736.12c
A:Map position: 3
A:Intons: 29/1; 349/1

Query Match 72.9%; Score 35; DB 2; Length 400;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 HDAPIG 6
| | | | |
DB 76 HDAPIG 81

RESULT 16
FK506-binding protein, FKBP51 - human
N:Alternate names: peptidyl prolyl cis-trans isomerase
C:Species: Homo sapiens (man)
C>Date: 10-Jun-1997 #sequence_revision 18-Jul-1997 #text_change 09-Jul-2004
C/Accession: J05422
R:Baughman, G.; Wederrecht, G.J.; Chang, F.; Martin, M.M.; Bourgeois, S.
Biochem. Biophys. Res. Commun. 232, 437-443, 1997
A:Title: Tissue distribution and abundance of human FKBP51, an FK506-binding protein the
A:Reference number: J05422; MUID:97242207; PMID:9125197
A/Accession: J05422
A:Molecule type: mRNA
A:Residues: 1-457 <BAU>
A/Cross-references: UNIPROT:Q13451, UNIPARC:UPI00000D9EE; GB:U71321; NID:G1916640; PIDR
A:Experimental source: thymus
C:Comment: This protein catalyzes the cis-to-trans isomerization of peptidyl-prolyl bond
C:Superfamily: human FK506-binding protein FKBP51; BKBP-type peptidylprolyl isomerase hc
F/50-97/Domain: BKBP-type peptidylprolyl isomerase homology <PPI>
F/317-350/Domain: tetratricopeptide repeat homology <TR1>
F/351-384/Domain: tetratricopeptide repeat homology <TR2>

Query Match 72.9%; Score 35; DB 2; Length 457;
Best Local Similarity 75.0%; Pred. No. 35;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 HDAPIG 8
| | | | |
DB 196 HDAPIG 203

RESULT 17
S45145
H+-transporting two-sector ATPase (EC 3.6.3.14) chain B [validated] - Haloflex volcanii
N:Alternate names: membrane ATPase
C/Species: Haloflex volcanii
C/Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 31-Dec-2004
C/Accession: S55896; S45145; T47204
R:Steinert, K.; Kroth-Pancic, P.G.; Bickel-Sandkoecker, S.
Biochim. Biophys. Acta 1249, 137-144, 1995
A:Title: Nucleotide sequence of the ATPase A- and B-subunits of the halophilic archaeobac
A:Reference number: S55896; MUID:95322432; PMID:7599166
A/Accession: S55896
A:Status: preliminary; nucleic acid sequence not shown
A:Molecule type: DNA
A/Residues: 1-468 <ST2>
A/Cross-references: UNIPROT:Q48333; UNIPARC:UPI000013815B; EMBL:X79516; NID:G693938; PID
A:Experimental source: strain WK340; unicellular; vegetative cells
C/Genetics:
A:Gene: atpB
A:Function:
A:Description: EC 3.6.3.14 [validated, MUID:97197793]
C:Superfamily: H(+)-transporting ATP synthase; H+-transporting ATP synthase alpha chain
C/Keywords: ATP biosynthesis; hydrolase; membrane-associated complex
F/183-354/Domain: H+-transporting ATP synthase alpha chain homology <ATP>

Query Match 72.9%; Score 35; DB 2; Length 468;
Best Local Similarity 85.7%; Pred. No. 36;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 DAPIG 8
| | | | |
DB 20 DAPIG 26

RESULT 18
S14733

H+-transporting two-sector ATPase (EC 3.6.3.14) beta chain [validated] - Halobacterium sa
C/Species: Halobacterium salinarum
C/Date: 21-Jul-2000 #sequence_revision 21-Jul-2000 #text_change 31-Dec-2004
C/Accession: S14733; S18499
R:Harra, K.; Mukohata, Y.
Arch. Biochem. Biophys. 286, 111-116, 1991
A:Title: The ATP synthase of Halobacterium salinarum (halobium) is an archaeobacterial ty
A:Reference number: S14732; MUID:91378275; PMID:1832829
A/Accession: S14733
A:Molecule type: DNA
A:Residues: 1-471 <IRA>
A/Cross-references: UNIPROT:P25164; UNIPARC:UPI000013815A; GB:X70294; GB:S56356; NID:G1434
A>Note: the source is given as Halobacterium salinarum
A/Accession: S18499
A:Molecule type: protein
A:Residues: 1-8;272-344;425-444;446-469 <IRA2>
A/Cross-references: UNIPARC:UPI0000172E22; UNIPARC:UPI0000172E23; UNIPARC:UPI0000172E24;
C/Genetics:
A:Gene: atpB
A:Complex: atpA (PIR:S14732) and atpB (PIR:S14733) are the head piece of the ATP synthase
C/Function:
A:Description: EC 3.6.3.14 [validated, PMID:9137827]
A>Note: the alpha chain is considered to be catalytic
C:Superfamily: H(+)-transporting ATP synthase; H+-transporting ATP synthase alpha chain
C/Keywords: ATP biosynthesis; hydrolase; membrane-associated complex; nucleotide binding
F/1-471/Product: H+-transporting ATP synthase beta chain #status experimental <MAT>
F/58-65/Region: nucleotide-binding motif A (P-loop)
F/186-357/Domain: H+-transporting ATP synthase alpha chain homology <ATP>

Query Match 72.9%; Score 35; DB 1; Length 471;
Best Local Similarity 85.7%; Pred. No. 36;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 DAPIG 8
| | | | |
DB 20 DAPIG 26

RESULT 19
H84363
H+-transporting ATP synthase subunit B [imported] - Halobacterium sp. NRC-1
C/Species: Halobacterium sp. NRC-1
C/Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 31-Dec-2004
C/Accession: H84363
R:Ng, W.V.; Kennedy, S.P.; Mahirae, G.G.; Bergius, B.; Pan, M.; Shukla, H.D.; Lasky, S
Jung, K.H.; Alam, M.; Pretias, T.
Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000
A:Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ehardt, H.; Lowe, T.M.; Lt
A:Title: Genome sequence of Halobacterium species NRC-1.
A:Reference number: A84160; MUID:20504483; PMID:11016950
A/Accession: H84363
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-471 <STO>
A/Cross-references: UNIPROT:Q9HNE4; UNIPARC:UPI0000138159; GB:AB004437; NID:G10581553; P
C/Genetics:
A:Gene: atpB

Query Match 72.9%; Score 35; DB 2; Length 471;
Best Local Similarity 85.7%; Pred. No. 36;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 DAPIG 8
| | | | |
DB 20 DAPIG 26

RESULT 20
A38368
Chitinase (EC 3.2.1.14) precursor - Bacillus circulans
C/Species: Bacillus circulans
C/Date: 28-Jun-1991 #sequence_revision 28-Jun-1991 #text_change 09-Jul-2004

C;Accession: A38368
R;Metanabe, T.; Suzuki, K.; Oyanagi, W.; Ohnishi, K.; Tanaka, H.
J. Biol. Chem. 265, 15659-15665, 1990
A;Title: Gene cloning of chitinase A1 from *Bacillus circulans* WL-12 revealed its evolution
A;Reference number: A38368; MUID:90368776; PMID:2203782
A;Accession: A38368
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-699 <WAT>
A;Cross-references: UNIPROT:P20533; UNIPARC:UPI00001277E5; GB:M57601; GB:J05599; NID:glc
C;Keywords: glycosidase; hydrolase; polyaccharide degradation

Query Match 72.9%; Score 35; DB 2; Length 699;
Best Local Similarity 62.5%; Pred. No. 55;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 HDAPIGYD 8
Db 291 HNAPLNYD 298

RESULT 21
A47296
thiazide-sensitive electroneutral sodium-chloride cotransporter - winter flounder
C;Species: *Pseudopleuronectes americanus* (winter flounder)
C;Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C;Accession: A47296
R;Gamba, G.; Saltzberg, S.N.; Lombardi, M.; Miyashita, A.; Lytton, J.; Hediger, M.A.;
Proc. Natl. Acad. Sci. U.S.A. 90, 2749-2753, 1993
A;Title: Primary structure and functional expression of a cDNA encoding the thiazide-ser
A;Reference number: A47296; MUID:93219361; PMID:8464884
A;Accession: A47296
A;Status: preliminary
A;Molecule type: nucleic acid
A;Residues: 1-1023 <GAM>
A;Cross-references: UNIPROT:P55019; UNIPARC:UPI000013541E
A;Experimental source: urinary bladder
A;Note: sequence extracted from NCB1 backbone (NCB1:128719, NCB1P:128720)
C;Superfamily: rat bumetanide-sensitive Na+/K+/Cl-cotransport protein

Query Match 72.9%; Score 35; DB 2; Length 1023;
Best Local Similarity 85.7%; Pred. No. 83;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 DAPIGYD 8
Db 52 DAPIGYD 58

RESULT 22
T06499
Rieske [2Fe-2S] iron-sulfur protein tic55 - garden pea
N;Alternate names: cell death suppressor protein homolog
C;Species: *Pisum sativum* (garden pea)
C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004
C;Accession: T06499
R;Callabe, A.; Grimm, R.; Kaiser, G.; Luebeck, J.; Soll, J.; Heins, L.
EMBO J. 16, 7342-7350, 1997
A;Title: The chloroplastic protein import machinery contains a Rieske-type iron-sulfur c
A;Reference number: 215721; MUID:98070311; PMID:9405363
A;Accession: T06499
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-553 <CAL>
A;Cross-references: UNIPROT:O49931; UNIPARC:UPI00000A1DAD; EMBL:AJ000520; NID:g2764523;
A;Experimental source: cultivar Golf
C;Genetics: tic55
C;Keywords: 2Fe-2S; chloroplastic; metalloprotein; Rieske iron-sulfur protein
F;144-181;Domain: Rieske [2Fe-2S] homology <RKS>
F;144,146,163,166;Binding site: 2Fe-2S cluster (Cys, His, Cys, His) (covalent) #status p

Query Match 71.9%; Score 34.5; DB 2; Length 553;

Best Local Similarity 63.6%; Pred. No. 54;
Matches 7; Conservative 1; Mismatches 0; Indels 3; Gaps 1;

Qy 1 HDAPIGYD 8
Db 114 HDAPLGLKXVD 124

RESULT 23
D71918
hypothetical protein jhp0550 - *Helicobacter pylori* (strain 399)
C;Species: *Helicobacter pylori*
A;Variety: strain 399
C;Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 09-Jul-2004
C;Accession: D71918
R;Alm, R.A.; Ling, L.S.L.; Moir, D.T.; King, B.L.; Brown, E.D.; Doty, P.C.; Smith, D.R.;
Ives, C.; Gibson, R.; Merberg, D.; Mills, S.D.; Jiang, Q.; Taylor, D.E.; Vovis, G.F.;
Nature 397, 176-180, 1999
A;Title: Genomic sequence comparison of two unrelated isolates of the human gastric path
A;Reference number: A71800; MUID:99120557; PMID:99233682
A;Accession: D71918
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-205 <ARN>
A;Cross-references: UNIPROT:Q9ZLM9; UNIPARC:UPI00000D71F9; GB:AE001487; GB:AE001439; NID
C;Experimental source: strain 399
A;Genes: jhp0550
C;Superfamily: *Helicobacter pylori* hypothetical protein jhp0550

Query Match 70.8%; Score 34; DB 2; Length 205;
Best Local Similarity 62.5%; Pred. No. 23;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 HDAPIGYD 8
Db 70 HDASLGFD 77

RESULT 24
S36706
B4 protein - equine herpesvirus 4
C;Species: equine herpesvirus 4
C;Date: 09-Jun-1994 #sequence_revision 12-May-1995 #text_change 09-Jul-2004
C;Accession: S36706
R;Rigbio, P.
submitted to the EMBL Data Library, November 1989
A;Reference number: S36703
A;Accession: S36706
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-290 <RIG>
A;Cross-references: UNIPROT:Q00039; UNIPARC:UPI0000137BBC; EMBL:X17684; NID:g2578026; PIR
C;Superfamily: varicella-zoster virus gene 9 protein

Query Match 70.8%; Score 34; DB 2; Length 290;
Best Local Similarity 100.0%; Pred. No. 34;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 APIGYD 8
Db 257 APIGYD 262

RESULT 25
T42554
tegument protein - equine herpesvirus 4 (strain NS80567)
C;Species: equine herpesvirus 4
A;Variety: strain NS80567
C;Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 09-Jul-2004
C;Accession: T42554
R;Telford, E.A.; Watson, M.S.; Perry, J.; Cullinane, A.A.; Davison, A.J.
J. Gen. Virol. 79, 1197-1203, 1998

A;Title: The DNA sequence of equine herpesvirus-4.
A;Reference number: 222173; MUID:98264497; PMID:9603335
A;Accession: T42554
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-304 <TEU>
A;Cross-references: UNIPROT:O39253; UNIPARC:UPI00000F2B2C; EMBL:AF030027; NID:G2605950;
A;Experimental source: strain NS80567
C;Genetics:
A;Gene: 11
C;Superfamily: varicella-zoster virus gene 9 protein

Query Match 70.8%; Score 34; DB 2; Length 304;
Best Local Similarity 100.0%; Pred. No. 36;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 3 APGYD 8
Db 271 APGYD 276

RESULT 26
T50960
related to modulation protein nodB [imported] - Neurospora crassa
N;Alternate names: protein B24P7.150
C;Species: Neurospora crassa
C;Date: 21-Jul-2000 #sequence_revision 21-Jul-2000 #text_change 09-Jul-2004
A;Accession: T50960
R;Schulze, U.; Aign, V.; Hohnesl, J.; Brandt, P.; Partmann, B.; Holland, R.; Nyakatura,
submitted to the Protein Sequence Database, July 2000
A;Reference number: 225286
A;Accession: T50960
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-312 <SCH>
A;Cross-references: UNIPROT:O993S0; UNIPARC:UPI000017B4FE; EMBL:AL389890; GSPDB:GN00116;
A;Experimental source: BAC clone B24P7; strain OK74A
C;Genetics:
A;Gene: NCSP:B24P7.150
A;Map position: 6

Query Match 70.8%; Score 34; DB 2; Length 312;
Best Local Similarity 85.7%; Pred. No. 37;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 HDAPGY 7
Db 249 HDAPGY 255

RESULT 27
T29810
hypothetical protein C46A5.3 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Sep-2003
A;Accession: T29810
R;Johnson, D.; Stellyes, L.
submitted to the EMBL Data Library, June 1996
A;Description: The sequence of C. elegans coamid C46A5.
A;Reference number: 220690
A;Accession: T29810
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-326 <JOH>
A;Cross-references: UNIPARC:UPI000017A120; EMBL:U61948; PIDD:AA03143.1; GSPDB:GN00022;
A;Experimental source: strain Bristol N2; clone C46A5
C;Genetics:
A;Gene: CESP:C46A5.3
A;Map position: 4
A;Introns: 91/2

Query Match 70.8%; Score 34; DB 2; Length 326;
Best Local Similarity 71.4%; Pred. No. 38;

Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
Qy 2 DAPGYD 8
Db 109 DQPGYD 115

RESULT 28
J50169
collagen col-14 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 15-Sep-2003
A;Accession: J50169
R;Cox, G.N.; Fields, C.; Kramer, J.M.; Rosenzweig, B.; Hirsch, D.
Gene 76, 331-344, 1989
A;Title: Sequence comparisons of developmentally regulated collagen genes of Caenorhabditis
A;Reference number: A91602; MUID:89326131; PMID:2753356
A;Accession: J50169
A;Molecule type: DNA
A;Residues: 1-326 <COX>
A;Cross-references: UNIPARC:UPI000016B8BD; GB:M25480; NID:G156251; PIDD:AAA27986.1; PID:G
C;Genetics:
A;Gene: col-14
A;Introns: 91/2
F;137-166/Domain: helical <HX1>
F;188-314/Domain: helical <HX2>

Query Match 70.8%; Score 34; DB 2; Length 326;
Best Local Similarity 71.4%; Pred. No. 38;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
Qy 2 DAPGYD 8
Db 109 DQPGYD 115

RESULT 29
AB2474
hypothetical protein al15346 [imported] - Nostoc sp. (strain PCC 7120)
C;Species: Nostoc sp. PCC 7120
A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004
A;Accession: AB2474
R;Kaneke, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Saeamoto, S.; Matsuda, A.; Itiguchi,
Nakazaki, N.; Shimo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Tabata, S.
DNA Res. 8, 205-213, 2001
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Anabaena
A;Reference number: AB1807; MUID:21595285; PMID:11759840
A;Accession: AB2474
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-392 <KUR>
A;Cross-references: UNIPROT:O8YLF2; UNIPARC:UPI00000C8E4D; GB:BA000019; PIDD:BA077045.1;
A;Experimental source: strain PCC 7120
C;Genetics:
A;Gene: al15346

Query Match 70.8%; Score 34; DB 2; Length 392;
Best Local Similarity 100.0%; Pred. No. 47;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 2 DAPGYD 7
Db 174 DAPGYD 179

RESULT 30
A96985
uncharacterized conserved protein, VanM of Enterococcus faecalis related CAC0691 [import
C;Species: Clostridium acetobutylicum
C;Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 09-Jul-2004
A;Accession: A96985
R;Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee,

.: Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.
J. Bacteriol. 183, 4823-4838, 2001
A>Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium C1C
A:Reference number: A96900; MUID:21355325; PMID:21359325
A:Accession: A96905
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-411 <KIR>
A:Cross-references: UNIPROT:Q97L71; UNIPARC:UPI00000C9F4F; GB:AE001437; P1DN:AAK78668.1;
A:Experimental source: Clostridium acetobutylicum ATCC824
C:Genetics:
A:Gene: CAC0691

Query Match 70.8%; Score 34; DB 2; Length 411;
Best Local Similarity 62.5%; Pred. No. 49;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 HDAPIGY 8
Db 319 HYVPGYD 326

RESULT 31
B64157
hypothetical protein HI0723 - Haemophilus influenzae (strain Rd KW20)
C:Species: Haemophilus influenzae
C>Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 18-Sep-1998
C:Accession: B64157
R:Feilschmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage, A.
R:Goeyne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodex, A.; Kelley, J.M.; Weidman, J.
D.M.; Brandon, R.C.; Fine, L.D.; Fritschman, J.L.; Fuhrmann, J.L.; Geoghagen, N.S.M.
Science 269, 496-512, 1995
A:Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraeger, C.M.; Smith, H.O.; Venter,
A>Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.
A:Reference number: A64000; MUID:95350630; PMID:7542800
A:Accession: B64157
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-423 <TIGR>
A:Cross-references: UNIPARC:UPI0000178DF; GB:U32755; GB:L42023; NID:91573722; P1D:91573
A>Note: best homolog was a hypothetical protein from Escherichia coli
C:Genetics:
A:Start codon: GTG
C:Superfamily: potassium uptake protein trkG

Query Match 70.8%; Score 34; DB 2; Length 423;
Best Local Similarity 85.7%; Pred. No. 51;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 HDAPIGY 7
Db 226 HDASIGY 232

RESULT 32
B65190
potassium uptake protein trkH [validated] - Escherichia coli (strain K-12)
C:Species: Escherichia coli
C>Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 09-Jul-2004
C:Accession: B65190; S30740; PC2366; A56151; JQ0754
R:Battner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Co
A:Rose, D.J.; Mau, B.; Siao, Y.
Science 277, 1453-1462, 1997
A>Title: The complete genome sequence of Escherichia coli K-12.
A:Reference number: A64720; MUID:97426617; PMID:9278503
A:Accession: B65190
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-432 <BLAT>
A:Cross-references: UNIPROT:P21166; UNIPARC:UPI00001681F8; GB:AE000460; GB:U00096; NID:9
A:Experimental source: strain K-12, substrain MG1655
R:Daifotis, D.L.; Plunkett III, G.; Burland, V.; Battner, F.R.
Science 257, 771-778, 1992

A>Title: Analysis of the Escherichia coli genome: DNA sequence of the region from 84.5 c
A:Reference number: S30660; MUID:92358234; PMID:1379743
A:Accession: S30740
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-68, 70-432 <DNA>
A:Cross-references: UNIPARC:UPI000016F69E; EMBL:M87049; NID:9836656; P1DN:AAA67646.1; P1L
A>Note: the nucleotide sequence was submitted to the EMBL Data Library, November 1992
R:Nishimura, K.; Nakayashiki, T.; Inokuchi, H.
DNA Res. 2, 1-8, 1995
A>Title: Cloning and identification of the hemG gene encoding protoporphyrinogen oxidase
A:Reference number: JQ2513; MUID:95308321; PMID:7788523
A:Accession: PC2366
A:Molecule type: DNA
A:Residues: 362-432 <NIS>
A:Cross-references: UNIPARC:UPI0000178E00
A:Experimental source: strain VSR751
R:Schloesser, A.; Meldorf, M.; Stumpe, S.; Bakker, E.P.; Epstein, W.
J. Bacteriol. 177, 1908-1910, 1995
A>Title: TrkH and its homolog, TrkG, determine the specificity and kinetics of cation tra
A:Reference number: A56151; MUID:95204366; PMID:7896723
A:Accession: A56151
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 1-417, 'TGVDD', 423, 'SAFASVATLNLGPGIGVADNFTSMNPVAKWILIANMLFGRLEVFLLVLPFTPTF
R:Nakagishi, K.; Inokuchi, H.
Nucleic Acids Res. 18, 6439, 1990
A>Title: Nucleotide sequence between the fadB gene and the rna operon from Escherichia c
A:Reference number: JQ0753; MUID:91057145; PMID:2243799
A:Accession: JQ0754
A:Molecule type: DNA
A:Residues: 1-143, 'T', 144-195, 'S', 197-419, 'G' <NAK>
A:Cross-references: UNIPARC:UPI0000178E01; EMBL:X54687
C:Genetics:
A:Gene: trkH
A:Map position: 86 min
C:Function:
A>Description: involved in potassium uptake [validated, MUID:95204366]
C:Superfamily: potassium uptake protein trkG
C:Keywords: transmembrane protein

Query Match 70.8%; Score 34; DB 2; Length 432;
Best Local Similarity 85.7%; Pred. No. 52;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 HDAPIGY 7
Db 226 HDASIGY 232

RESULT 33
A91226
potassium uptake protein [imported] - Escherichia coli (strain O157:H7, substrain R1MD 05
C:Species: Escherichia coli
C>Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 09-Jul-2004
C:Accession: A91226
R:Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.
gasawara, N.; Yasunaga, T.; Kuhnara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001
A>Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and genom
A:Reference number: A96629; MUID:21156231; PMID:11258796
A:Accession: A91226
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-483 <HAY>
A:Cross-references: UNIPROT:P21166; UNIPARC:UPI00001373D1; GB:BA000007; P1DN:BA838200.1;
A:Experimental source: strain O157:H7, substrain R1MD 0509952
C:Genetics:
A:Gene: EC84777
C:Superfamily: potassium uptake protein trkG

Query Match 70.8%; Score 34; DB 2; Length 483;

Best Local Similarity 85.7%; Pred. No. 59;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 HDAPIGY 7
Db 226 HDASIGY 232

RESULT 34
G86072
potassium uptake protein, requires TrkE [imported] - *Escherichia coli* (strain O157:H7, 8
C/Species: *Escherichia coli*
C/Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
C/Accession: G86072
R/Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew
Miller, L.; Grobeck, E.J.; Davis, N.W.; Lam, A.; Dimalanta, E.; Potamousis, K.; Apodaca,
Nature 409, 529-533, 2001
A/Title: Genome sequence of enterohemorrhagic *Escherichia coli* O157:H7.
A/Reference number: AB5460; MUID:21074935; PMID:11206551
A/Accession: G86072
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-483 <STO>
A/Cross-references: UNIPROT:P21166; UNIPARC:UPI00001373D1; GB:AE005174; NID:g12518727; F
A/Experimental source: strain O157:H7, substrain EDL933
C/Genetics:
A/Gene: trkH
C/Superfamily: potassium uptake protein trkG

Query Match 70.8%; Score 34; DB 2; Length 483;
Best Local Similarity 85.7%; Pred. No. 59;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 HDAPIGY 7
Db 226 HDASIGY 232

RESULT 35
AB0458
Trk system potassium uptake protein TrkH [imported] - *Yersinia pestis* (strain CO92)
C/Species: *Yersinia pestis*
C/Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Jul-2004
C/Accession: AB0458
R/Parkhill, J.; Wren, B.W.; Thomson, N.R.; Tlhalil, R.W.; Holden, M.T.G.; Prentice, M.B.
deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.;
ll, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrett,
Nature 413, 523-527, 2001
A/Title: Genome sequence of *Yersinia pestis*, the causative agent of plague.
A/Reference number: AB0001; MUID:21470413; PMID:11586360
A/Accession: AB0458
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-483 <KUR>
A/Cross-references: UNIPROT:O8ZAN2; UNIPARC:UPI00000DC896; GB:AL590842; PIDN:CA093230.1;
C/Genetics:
A/Gene: trkH
C/Superfamily: potassium uptake protein trkG

Query Match 70.8%; Score 34; DB 2; Length 483;
Best Local Similarity 85.7%; Pred. No. 59;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 HDAPIGY 7
Db 226 HDASIGY 232

RESULT 36
D84942
methionine-tRNA ligase (EC 6.1.1.10) [imported] - *Buchnera* sp. (strain APS)
N/Alternate names: methionyl-tRNA synthetase
C/Species: *Buchnera* sp.

C/Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 17-Feb-2003
C/Accession: D84942
R/Shigenobu, S.; Watanabe, H.; Hattori, M.; Sakaki, Y.; Ishikawa, H.
Nature 407, 81-86, 2000
A/Title: Genome sequence of the endocellular bacterial symbiont of aphids *Buchnera* sp. At
A/Reference number: AB4930; MUID:20445173; PMID:10993077
A/Accession: D84942
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-547 <STO>
A/Cross-references: UNIPARC:UPI000005846F; GB:AP000398; GSPDB:GN00144
A/Experimental source: strain APS
C/Genetics:
A/Gene: metG, BU109
C/Superfamily: methionyl-tRNA synthetase
C/Keywords: ligase

Query Match 70.8%; Score 34; DB 2; Length 547;
Best Local Similarity 100.0%; Pred. No. 67;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 2 DAPIGY 7
Db 256 DAPIGY 261

RESULT 37
H81718
methionyl-tRNA synthetase TC0301 [imported] - *Chlamydia muridarum* (strain N199)
C/Species: *Chlamydia muridarum*, *Chlamydia trachomatis* Mopn
C/Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004
C/Accession: H81718
R/Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hickey, J.
C.; Dodson, R.; Gwinn, M.; Nelson, W.; Deboy, R.; Kolonay, J.; McClarty, G.; Salzberg,
Nucleic Acids Res. 28, 1397-1406, 2000
A/Title: Genome sequences of *Chlamydia trachomatis* Mopn and *Chlamydia pneumoniae* AR39.
A/Reference number: AB1500; MUID:20150255; PMID:10684935
A/Accession: H81718
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-550 <TEB>
A/Cross-references: UNIPROT:Q9PL07; UNIPARC:UPI000005788D; GB:AE002297; GB:AE002160; NID
A/Experimental source: strain N199 (MOPn)
C/Genetics:
A/Gene: TC0301
C/Superfamily: methionyl-tRNA synthetase

Query Match 70.8%; Score 34; DB 2; Length 550;
Best Local Similarity 100.0%; Pred. No. 67;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 2 DAPIGY 7
Db 253 DAPIGY 258

RESULT 38
C71567
methionine-tRNA ligase (EC 6.1.1.10) - *Chlamydia trachomatis* (serotype D, strain UM3/Cx)
C/Species: *Chlamydia trachomatis*
C/Date: 13-Sep-1998 #sequence_revision 13-Sep-1998 #text_change 09-Jul-2004
C/Accession: C71567
R/Stephens, R.S.; Kaiman, S.; Lammel, C.J.; Fan, J.; Marathe, R.; Aravind, L.; Mitchell,
Science 282, 754-759, 1998
A/Title: Genome sequence of an obligate intracellular pathogen of humans: *Chlamydia trach*
A/Reference number: A71570; MUID:99000809; PMID:9784136
A/Accession: C71567
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-550 <ARN>
A/Cross-references: UNIPROT:O84035; UNIPARC:UPI0000047BF6; GB:AE001277; GB:AE001273; NID
A/Experimental source: serotype D, strain UM-3/Cx
C/Genetics:

Job time : 40 secs

A:Gene: metG
C:Superfamily: methionyl-tRNA synthetase
C:Keywords: aminocyl-tRNA synthetase; ligase; protein biosynthesis

Query Match 70.8%; Score 34; DB 2; Length 550;
Best Local Similarity 100.0%; Pred. No. 67;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 DAPIGY 7
|||||
Db 253 DAPIGY 258

RESULT 39

H72117
methionine-tRNA ligase (EC 6.1.1.10) - Chlamydia pneumoniae (strain CWL029)
C:Species: Chlamydia pneumoniae, Chlamydia pneumoniae
C:Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004
C:Accession: H72117
R:Kaitman, S.; Mitchell, W.; Marathe, R.; Lammel, C.; Fan, J.; Olinger, L.; Grimwood, J.;
Nature Genet. 21, 385-389, 1999
A:Title: Comparative genomes of Chlamydia pneumoniae and C. trachomatis.
A:Reference number: A72000; MUID:99206606; PMID:10192388
A:Accession: H72117
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-551 <ARN>
A:Cross-references: UNIPROT:Q92959, UNIPARC:UPI0000165616, GB:AE001598, GB:AE001363, NID
A:Experimental source: strain CWL029
C:Genetics:
A:Gene: metG
C:Superfamily: methionyl-tRNA synthetase
C:Keywords: aminocyl-tRNA synthetase; ligase; protein biosynthesis

Query Match 70.8%; Score 34; DB 2; Length 551;
Best Local Similarity 100.0%; Pred. No. 68;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 DAPIGY 7
|||||
Db 252 DAPIGY 257

RESULT 40

C86506:
methionyl-tRNA synthetase [imported] - Chlamydia pneumoniae (strain J138)
C:Species: Chlamydia pneumoniae, Chlamydia pneumoniae
C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C:Accession: C86506
R:Shirai, M.; Hirakawa, H.; Kimoto, M.; Tsubuchi, M.; Kishi, F.; Ouchi, K.; Shiba, T.; Ie
Nucleic Acids Res. 28, 2311-2314, 2000
A:Title: Comparison of whole genome sequences of chlamydia pneumoniae J138.
A:Reference number: A86491; MUID:20330349; PMID:10871362
A:Accession: C86506
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-551 <STO>
A:Cross-references: UNIPROT:Q92959, UNIPARC:UPI000013658B, GB:BA000008, NID:g8978496, PI
A:Experimental source: strain J138
C:Genetics:
A:Gene: metG
C:Superfamily: methionyl-tRNA synthetase

Query Match 70.8%; Score 34; DB 2; Length 551;
Best Local Similarity 100.0%; Pred. No. 68;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 DAPIGY 7
|||||
Db 252 DAPIGY 257

Search completed: December 3, 2005, 23:29:13

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OM protein - protein search, using sw model

Run on: December 3, 2005, 23:28:09 ; Search time 226 Seconds
(without alignments)
24.974 Million cell updates/sec

Title: US-10-807-553-2
Perfect score: 48
Sequence: 1 HDAPIGYD 8

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues
Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Listing first 100 summaries

Database : Uniprot 05.80:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	48	100.0	125	2	08C944 MOUSE
2	48	100.0	735	1	KPCE_RABIT
3	48	100.0	737	1	KPCE_HUMAN
4	48	100.0	737	1	KPCE_MOUSE
5	48	100.0	737	1	KPCE_RAT
6	48	100.0	737	2	06DUV1 RAT
7	48	100.0	754	2	04SGH8 TETNG
8	48	100.0	895	2	04T021 TETNG
9	44	91.7	118	2	04TFB5 TETNG
10	44	91.7	766	2	04RM42 TETNG
11	41	85.4	774	2	08D965 VIBVU
12	41	85.4	800	2	07MLA7 VIBVU
13	40	83.3	887	2	06GNZ7 XENLA
14	39	81.2	421	2	06N9D6 RHOPA
15	39	81.2	586	2	08H055 ORISA
16	39	81.2	652	2	06O070 SCHPO
17	39	81.2	731	2	08H922 ORYSA
18	39	81.2	861	2	05S0S2 CRYNE
19	39	81.2	861	2	05KFE2 CRYNE
20	39	81.2	869	2	04A126 XENLA
21	39	81.2	869	2	06NS01 XENLA
22	38	79.2	121	2	07IUV9 HUMAN
23	38	79.2	682	1	KPCL_HUMAN
24	38	79.2	683	1	KPCL_MOUSE
25	38	79.2	683	1	KPCL_RAT
26	38	79.2	683	1	08NE03 HUMAN
27	38	79.2	683	2	08K2K8 MOUSE
28	38	79.2	1025	1	POZ1_NASVI
29	37	77.1	493	2	04KB20 PSEFS
30	37	77.1	493	2	04A320 HIPCN
31	37	77.1	685	2	04PGX8 USTMA

32	37	77.1	695	2	091WX8 RAT	091WX8 ratus norv
33	37	77.1	2203	1	CACID RAT	P27732 ratus norv
34	36	75.0	213	2	06D719 ERWCT	06D719 erwila car
35	36	75.0	229	2	08U340 XENLA	08U340 xenopus lae
36	36	75.0	461	2	04PD5 USTVA	04PD5 ustlago ma
37	35	72.9	66	2	06S631 ORYSA	06S631 oryza sativ
38	35	72.9	171	2	09F5F3 AGRRH	09F5F3 agrobacteri
39	35	72.9	180	2	09LZG9 ARATH	09LZG9 arabidopsis
40	35	72.9	199	2	09R6J9 PRHIZ	09R6J9 agrobacteri
41	35	72.9	199	2	08U626 AGRRS	08U626 agrobacteri
42	35	72.9	218	2	08XHB1 CLOPE	08XHB1 clostridium
43	35	72.9	226	2	04L708 STAPU	04L708 staphylococ
44	35	72.9	229	2	08FBL7 ECOL6	08FBL7 escherichia
45	35	72.9	233	2	07ZXG7 XENLA	07ZXG7 xenopus lae
46	35	72.9	238	2	04FT28 GAWMW	04FT28 psychrobact
47	35	72.9	257	2	0726G2 DESVH	0726G2 desulfovibr
48	35	72.9	260	2	08KX57 STRWM	08KX57 streptomyce
49	35	72.9	267	2	059EB8 HUMAN	059EB8 homo sapien
50	35	72.9	300	2	05VKR1 SACER	05VKR1 saccharopol
51	35	72.9	336	2	05ZKV1 CHICK	05ZKV1 gallus gall
52	35	72.9	351	2	062BK2 CAERL	062BK2 caenorhabdi
53	35	72.9	371	2	09NAM5 CAERL	09NAM5 caenorhabdi
54	35	72.9	385	2	08S0S1 ORYSA	08S0S1 oryza sativ
55	35	72.9	402	2	08KNG9 MICEC	08KNG9 micromosp
56	35	72.9	432	2	074958 SCHPO	074958 schizosacch
57	35	72.9	449	2	0646T7 CHICK	0646T7 gallus gall
58	35	72.9	456	1	FKBP5 MOUSE	064378 mus musculu
59	35	72.9	456	2	06ZR21 HUMAN	06ZR21 homo sapien
60	35	72.9	456	2	05U2T9 RAT	05U2T9 ratus norv
61	35	72.9	456	2	04F0N2 MOUSE	04F0N2 mus musculu
62	35	72.9	457	1	FKBP5 AOTNA	09X11 actue nancy
63	35	72.9	457	1	FKBP5 CERNA	09X10 ceropichne
64	35	72.9	457	1	FKBP5 HUMAN	013451 h.fk506-bin
65	35	72.9	457	1	FKBP5 SNGOE	09X612 saguinus oe
66	35	72.9	457	1	FKBP5 SATIB	09X615 salmuri bol
67	35	72.9	457	2	05TGM6 HUMAN	05TGM6 homo sapien
68	35	72.9	457	2	053GX4 HUMAN	053GX4 homo sapien
69	35	72.9	468	1	VATR_HALVO	048333 halobacteri
70	35	72.9	471	1	VATR_HALVA	09Hn64 halobacteri
71	35	72.9	483	2	067B65 GCHUR	067B65 dehalococco
72	35	72.9	552	2	04H2P4 GIBZE	04H2P4 gibberella
73	35	72.9	581	2	07SAF7 NEURB	07SAF7 neurospora
74	35	72.9	591	2	05EB14 VIBF1	05EB14 vibrio fisc
75	35	72.9	611	2	08DDZ2 VIBVU	08DDZ2 vibrio vuln
76	35	72.9	611	2	07MPR4 VIBVU	07MPR4 vibrio vuln
77	35	72.9	644	2	08CWN1 STAPD	08CWN1 staphylococ
78	35	72.9	644	2	05HMH0 STABO	05HMH0 staphylococ
79	35	72.9	657	2	063KY9 BURPA	063KY9 burkholderi
80	35	72.9	657	2	062C50 BURPA	062C50 burkholderi
81	35	72.9	699	1	CHIA1_BACCI	P05533 bacillus ci
82	35	72.9	785	2	0869D8 ASCCS	0869D8 aciditla syd
83	35	72.9	795	2	053N63 ORYSA	053N63 oryza sativ
84	35	72.9	924	1	GLNB_ACIAD	08F619 actinobact
85	35	72.9	943	2	07S3J2 NEUCR	07S3J2 neurospora
86	35	72.9	1023	1	512A3_PSEAM	P55019 pseudopleur
87	35	72.9	1429	2	05G254 BRARE	05G254 brachydanio
88	34.5	71.9	553	2	049931_PBA	049931 pismu sativ
89	34	70.8	148	2	063OD5 BURPS	063OD5 burkholderi
90	34	70.8	156	2	084KX1 GASPA	084KX1 crocus sati
91	34	70.8	177	2	09EUW4 LISIN	09EUW4 listeria in
92	34	70.8	180	2	062G44 BURMA	062G44 burkholderi
93	34	70.8	183	2	04L145 9BURK	04L145 burkholderi
94	34	70.8	194	2	06M0G1 METWP	06M0G1 methanococc
95	34	70.8	205	2	09ZLM9 HELPD	09ZLM9 helicobacte
96	34	70.8	216	2	072VFI_LEPIC	072VFI leptospira
97	34	70.8	216	2	08CXU6 LEPTC	08CXU6 leptospira
98	34	70.8	221	2	041606 GIBZE	041606 gibberella
99	34	70.8	222	2	06C524 YARLI	06C524 yarrowia li
100	34	70.8	223	2	08F4F3_LEPIN	08F4F3 leptospira

ALIGNMENTS

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RESULT 1
08C944 MOUSE PRELIMINARY; PRT; 125 AA.
ID 08C944
AC 08C944
DT 01-MAR-2003 (TREMblrel. 23, Created)
DT 01-MAR-2003 (TREMblrel. 26, Last annotation update)
DE Mus musculus 7 days neonate cerebellum cDNA, RIKEN full-length
DE enriched library, clone:A730046G04 product:protein kinase C, epsilon,
DE full insert sequence.
GN Name=Prkce;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Cerebellum;
RX Medline=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Arch. Enzymol. 303:19-44(1999).
421
RN NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Cerebellum;
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Kono H., Adachi J., Fukuda S.,
RA Aizawa K., Iizawa M., Nishi K., Kiyosawa H., Kondo S., Yamanka I.,
RA Saito T., Okazaki Y., Gojodori T., Bono H., Kaubekawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Maceno Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schirni L.M., Struhl F., Suzuki R., Tomita M., Wagner L., Watanabe T.,
RA Sakai K., Okubo T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boileau D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bull C., Fletcher C., Fujita M., Gariboldi M.,
RA Guestinich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombere P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoedach C., Seta T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyokawa K., Wang K.H., Weitz C., Whitaker C., Wilming L.,
RA Wyszewski-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kontani S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
3
RN NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Cerebellum;
RA The FANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
4
RN NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Cerebellum;
RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Kono H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630(2000).
5
RN NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Cerebellum;
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagaoaka S., Sasaki N., Carninci P.,
RA Kono H., Akiyama J., Nishi K., Kitsuai T., Taahiro H., Itoh M.,
RA Suni N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada K.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,

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RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Matsuki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsumura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771(2000).
6
RN NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Cerebellum;
RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume M.,
RA Hayashida K., Hayatsu N., Hiramoto K., Hirooka T., Hirozane T.,
RA Hori F., Imocani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
RA Katoh H., Kawai J., Kojima Y., Kondo S., Kono H., Kouda M., Koya S.,
RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA Nishi K., Nomura K., Numazaki R., Ono M., Ohsato N., Okazaki Y.,
RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
RA Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
CC -1-SIMILARITY: Contains 1 C2 domain.
DR EMBL; AK042994; BAC1430.1; -, mRNA.
DR HSPD; P09216; IGMI.
DR SMK; Q8C944; 1-116.
DR Ensembl; ENSMUSG00000045038; Mus musculus.
DR MGJ; MGJ:97559; Prkce.
DR GO; GO:0016301; F:kinase activity; IEA.
DR InterPro; IPR000008; C2.
DR Pfam; PF00168; C2; 1.
DR PRINTS; PR00360; C2DOMAIN.
DR SMART; SM00239; C2; 1.
DR PROSITE; PS50004; C2_DOMAIN_2; 1.
KW Kinase.
SQ
SEQUENCE 125 AA; 14137 MW; 585D11F6BFC5C5 CRC64;
Query Match 100.0%; Score 48; DB 2; Length 125;
Best Local Similarity 100.0%; Pred. No. 0.088;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 HDAPIGYD 8
DB 85 HDAPIGYD 92
RESULT 2
KPCE RABIT STANDARD; PRT; 736 AA.
ID KPCE RABIT
AC P10830;
DT 01-JUL-1989 (Rel. 11, Created)
DT 01-JUL-1989 (Rel. 11, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Protein kinase C, epsilon type (BC 2.7.1.-) (PKC-epsilon).
GN Name=PRKCE; cuniculus (Rabbit).
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Lagomorpha; Leporidae;
OC Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP NUCLEOTIDE SEQUENCE (mRNA).
RC MEDLINE=88223367; PubMed=3370672; DOI=10.1016/0092-8674(88)90091-8;
RX Ohno S., Akita Y., Kono Y., Imaoh S., Suzuki K.;
RA "A novel phospholipid receptor/protein kinase, nPKC, distantly
RT related to the protein kinase C family.";
RL Cell 53:731-741(1988).
CC -1- FUNCTION: This is calcium-independent, phospholipid-dependent,
CC serine- and threonine-specific enzyme.
CC -1- FUNCTION: PKC is activated by diacylglycerol which in turn
CC phosphorylates a range of cellular proteins. PKC also serves as
CC the receptor for phospholipids, a class of tumor promoters.
CC -1- PTM: Phosphorylation on Thr-565 triggers autophosphorylation on
CC Ser-728 (by similarity).

```

CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family. PKC subfamily.
 CC -1- SIMILARITY: Contains 1 C2 domain.
 CC -1- SIMILARITY: Contains 2 phorbol-ester/DAG-type zinc fingers.
 CC -----
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 CC -----
 DR EMBL; M20014; AAA31426.1; -; mRNA.
 DR HSSP; P09216; 1GMI.
 DR SMR; P10830; 1-136.
 DR InterPro; IPR000008; C2.
 DR InterPro; IPR002219; DAG_pe_bd.
 DR InterPro; IPR000961; Pkinase_C.
 DR InterPro; IPR000719; Prot_kinase.
 DR InterPro; IPR008271; Ser_thr_pkin_AS.
 DR InterPro; IPR002290; Ser_thr_pkinase.
 DR Pfam; PF00130; C1.1; 2.
 DR Pfam; PF00168; C2; 1.
 DR Pfam; PF00069; Pkinase; 1.
 DR Pfam; PF00433; Pkinase_C; 1.
 DR PRINTS; PR00360; C2DOMAIN.
 DR PRINTS; PR00008; DAGPDOMAIN.
 DR PRODOM; PD000001; Prot_kinase; 1.
 DR SMART; SM00109; C1; 2.
 DR SMART; SM00239; C2; 1.
 DR SMART; SM00133; S_TK_X; 1.
 DR SMART; SM00220; S_TKC; 1.
 DR PROSITE; PS50004; C2 DOMAIN; 1.
 DR PROSITE; PS50107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
 DR PROSITE; PS00479; ZF_DAG_pe_1; 1.
 DR PROSITE; PS50081; ZF_DAG_pe_2; 2.
 KW ATP-binding; Kinase; Metal-binding; Nucleotide-binding;
 KW Phorbol-ester-binding; Phosphorylation; Repeat;
 KW Serine/threonine-protein kinase; Transferase; Zinc; Zinc-finger.
 FT DOMAIN 1 99 C2.
 FT ZN_FING 407 667 Phorbol-ester/DAG-type 1.
 FT ZN_FING 169 220 Phorbol-ester/DAG-type 2.
 FT NP_BIND 242 292 ATP (By similarity).
 FT ACT_SITE 413 421 Proton acceptor (By similarity).
 FT BINDING 531 531 ATP (By similarity).
 FT MOD_RES 436 436 Phosphothreonine (By similarity).
 FT MOD_RES 565 565 Phosphothreonine (by autocatalysis) (Potential).
 FT MOD_RES 702 702 Phosphothreonine (by autocatalysis) (Potential).
 FT MOD_RES 709 709 Phosphothreonine (by autocatalysis) (Potential).
 FT MOD_RES 728 728 Phosphoserine (by autocatalysis) (By similarity).
 SQ SEQUENCE 736 AA; 83516 MW; 261C4FE59B9BFB CRC64;
 Query Match 100.0%; Score 48; DB 1; Length 736;
 Best Local Similarity 100.0%; Pred. NO. 0.59;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Gy 1 HDAPIGVD 8
 Db 85 HDAPIGVD 92
 RESULT 3
 KPCE HUMAN STANDARD; PRT; 737 AA.
 AC 002156; Q53SL4; Q53SM5; Q9UEB1;
 DT 01-JUL-1993 (Rel. 26; Created)
 DT 01-JUL-1993 (Rel. 26; Last sequence update)
 DT 13-SEP-2005 (Rel. 48; Last annotation update)
 DE Protein kinase C, epsilon type (EC 2.7.1.-) (mKC-epsilon).

GN Name=PKCE; Synonyms=PKCE;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
 OC Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE [MRNA].
 RX MEDLINE=93003318; PubMed=1382605; DOI=10.1016/0167-4781(92)90006-L;
 RA Barts P., Strickland M.B., Holmes W., Loomis C.R., Ballas L.M.,
 RA Burns D.J.
 RT "Sequence and expression of human protein kinase C-epsilon.";
 RL Biochem. Biophys. Acta 1132:154-160(1992).
 RN [2]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA] OF 1-354 AND 480-737.
 RX PubMed=1815621; DOI=10.1038/nature03466;
 RA Hillier L.W., Graves T.A., Fulton R.S., Fulton L.A., Pegin K.H.,
 RA Muz P., Wagner-McPherson C., Layman D., Wyllie K., Sekhon M.,
 RA Becker M.C., Fewell G.A., Delehaunty K.D., Miner T.L., Nash W.E.,
 RA Kremetzki C., Oddy L., Du H., Sun H., Bradshaw-Cordum H., Ali J.,
 RA Carter J., Cordes M., Harris A., Isak A., van Brunt A., Nguyen C.,
 RA Du F., Courtney L., Kalicki J., Ozersky P., Abbott S., Armstrong J.,
 RA Belter E.A., Caruso L., Cedroni M., Colton M., Davidson T., Desai A.,
 RA Elliott G., Erb T., Fronick C., Gaige T., Haakenson W., Haglund K.,
 RA Holmes A., Harkins R., Kim K., Kruchowski S.S., Strong C.M.,
 RA Holmes A., Goyes E., Hou S., Levy A., Martinka S., Mead K.,
 RA McCellan M.D., Meyer R., Randall-Maher J., Tomlinson C.,
 RA Dauphin-Kohlberg S., Kozlowski-Reilly A., Shah N.,
 RA Swearingen-Shahid S., Snider J., Strong J.T., Thompson J., Yeakum M.,
 RA Leonard S., Pearson C., Trant L., Radionenko M., Waligorski J.E.,
 RA Wang C., Rock S.M., Tin-Wollam A.-M., Maupin R., Latreille P.,
 RA Wendt M.C., Yang S.-P., Pohl C., Wallis J.W., Speith J., Bieri T.A.,
 RA Berkowicz N., Nelson J.O., Osborne J., Ding L., Meyer R., Sabo A.,
 RA Shokland Y., Stihna P., Wohldmann P.B., Cook L.L., Hickenbotham M.T.,
 RA Eldred J., Williams D., Jones T.A., She X., Ciccarelli F.D., Huang X.,
 RA Izaurralde E., Taylor J., Schmutz J., Myers R.M., Cox D.R., Huang X.,
 RA McPherson J.D., Mardis E.R., Clifton S.W., Warren W.C.,
 RA Chinwalla A.T., Eddy S.R., Marra M.A., Ovcharenko I., Frey T.S.,
 RA Miller W., Eichler E.E., Bork P., Suyama M., Torrents D.,
 RA Waterston R.H., Wilson R.K.;
 RT "Generation and annotation of the DNA sequences of human chromosomes 2 and 4.";
 RL Nature 434:724-731(2005).
 RN [3]
 RP PHOSPHORYLATION SITES THR-566 AND SER-729, AND MUTAGENESIS OF LYS-437;
 RP THR-566; THR-710 AND SER-729.
 RX MEDLINE=2196415; PubMed=11964154; DOI=10.1042/0264-6021:3630537;
 RA Cenni V., Doeppler H., Sonnenburg E.D., Maraldi N., Newton A.C.,
 RA Toker A.;
 RT "Regulation of novel protein kinase C epsilon by phosphorylation.";
 RL Biochem. J. 363:537-545(2002).
 CC -1- FUNCTION: This is calcium-independent, phospholipid-dependent, serine- and threonine-specific enzyme.
 CC -1- FUNCTION: PKC is activated by diacylglycerol which in turn phosphorylates a range of cellular proteins. PKC also serves as the receptor for phorbol esters, a class of tumor promoters.
 CC -1- PFM: Phosphorylation on Thr-566 by PDPK1 triggers autophosphorylation on Ser-729.
 CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family. PKC subfamily.
 CC -1- SIMILARITY: Contains 1 C2 domain.
 CC -1- SIMILARITY: Contains 2 phorbol-ester/DAG-type zinc fingers.
 CC -----
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 CC -----
 DR EMBL; X65293; CAA46388.1; -; mRNA.
 DR EMBL; U51244; AAD08855.1; -; Genomic DNA.
 DR EMBL; AC017078; AAY44773.1; -; Genomic DNA.
 DR EMBL; AC017006; AAX93253.1; -; Genomic DNA.

DR PIR; S28942; S28942.
 DR HSSP; P09216; 1GMI.
 DR SMR; Q02156; 1-136.
 DR Ensemble; ENSG00000171132; Homo sapiens.
 DR HGNC; HGNC:9401; PRKCE.
 DR H-INVD; HIX0019150; -.
 DR MIM; 176975; -.
 DR GO; GO:0005624; C:membrane fraction; TAS.
 DR GO; GO:0004697; F:protein kinase C activity; TAS.
 DR GO; GO:0004871; F:signal transducer activity; TAS.
 DR GO; GO:0006917; P:induction of apoptosis; TAS.
 DR GO; GO:0006468; P:protein amino acid phosphorylation; TAS.
 DR GO; GO:0007165; P:signal transduction; TAS.
 DR InterPro; IPR000008; C2.
 DR InterPro; IPR002219; DAG_Pe_bd.
 DR InterPro; IPR000961; Kinase_C.
 DR InterPro; IPR000719; Prot_kinase.
 DR InterPro; IPR008271; Ser_thr_pkin_AS.
 DR InterPro; IPR002290; Ser_thr_pkinase.
 DR Pfam; PF00130; C1_1; 2.
 DR Pfam; PF00168; C2_1.
 DR Pfam; PF00069; Kinase; 1.
 DR Pfam; PF00433; Kinase_C; 1.
 DR PRINTS; PR00360; C2DOMAIN.
 DR PRINTS; PR00008; DAGPEDOMAIN.
 DR PRODOM; PD000001; Prot_kinase; 1.
 DR SMART; SM00109; C1; 2.
 DR SMART; SM00239; C2; 1.
 DR SMART; SM00133; S_TK_X; 1.
 DR SMART; SM00220; S_TKC; 1.
 DR PROSITE; PS50004; C2 DOMAIN; 1.
 DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
 DR PROSITE; PS50011; PROTEIN KINASE DOM; 1.
 DR PROSITE; PS00108; PROTEIN KINASE ST; 1.
 DR PROSITE; PS00479; ZF_DAG_Pe_1; 2.
 DR PROSITE; PS50081; ZF_DAG_Pe_2; 2.
 DR ATP-binding; Kinase; Metal-binding; Nucleotide-binding;
 KW Phorbol-ester binding; Phosphorylation; Repeat;
 KW Serine/threonine-protein kinase; Transferase; Zinc; Zinc-finger.
 FT DOMAIN 1 99 C2.
 FT ZN_FING 408 668 Protein kinase.
 FT ZN_FING 242 220 Phorbol-ester/DAG-type 1.
 FT NP_BIND 242 292 Phorbol-ester/DAG-type 2.
 FT ACT_SITE 414 422 ATP (By similarity).
 FT BINDING 532 532 Proton acceptor (By similarity).
 FT MOD_RES 437 437 ATP (By similarity).
 FT MOD_RES 566 566 Phosphothreonine (by PDPL).
 FT MOD_RES 703 703 Phosphothreonine (by autocatalysis) (potential).
 FT MOD_RES 710 710 Phosphothreonine (by autocatalysis) (potential).
 FT MOD_RES 729 729 Phosphoserine (by autocatalysis).
 FT MOD_RES 437 437 K->W. Abolishes activity and S-729 phosphorylation.
 FT MUTAGEN 566 566 T->A: Abolishes phosphorylation by PDK1, and S-729 phosphorylation.
 FT MUTAGEN 566 566 T->E: No effect on S-729 phosphorylation.
 FT MUTAGEN 710 710 T->E: No effect on activity; no effect on S-729 phosphorylation.
 FT MUTAGEN 729 729 S->A: Enhances T-566 dephosphorylation.
 SQ SEQUENCE 737 AA; 83674 MW; 85032DDA091A1F7 CRC64;

Query Match 100.0%; Score 48; DB 1; Length 737;
 Best local similarity 100.0%; Pred. No. 0.6;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 HDAPICGD 8
 DB 85 HDAPICGD 92

RESULT 4
 KPCE_MOUSE

ID KPCE_MOUSE STANDARD; PRT; 737 AA.
 AC P16054;
 DT 01-APR-1990 (Rel. 14, Created)
 DT 01-APR-1990 (Rel. 14, Last sequence update)
 DT 13-SEP-2005 (Rel. 48, Last annotation update)
 DE Protein kinase C, epsilon type (EC 2.7.1.1-) (PKC-epsilon).
 GN Name=Pkce; Synonym=Pkce; Pkceae;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Muridae; Murinae; Mus.
 OX NCBI_TaxId=10090;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=99137541; PubMed=2917656; DOI=10.1016/0014-5793(89)80160-7;
 RA Schaap D., Parker P.J., Bristol A., Kitz R., Knopf J.;
 RT "Unique substrate specificity and regulatory properties of PKC-
 epsilon: a rationale for diversity.";
 RT FEBS Lett. 243:351-357(1989).
 RL [2]
 RN NUCLEOTIDE SEQUENCE.
 RP TISSUE=Brain;
 RX MEDLINE=98127436; PubMed=9467942; DOI=10.1038/sj.onc.1201507;
 RA Wang Q.J., Ace P., Goodnight J., Blumberg P.M., Mischak H.,
 RA Mushinski J.F.;
 RT "The catalytic domain of PKC-epsilon, in reciprocal PKC-delta and -
 epsilon chimeras, is responsible for conferring tumorigenicity to
 NIH3T3 cells, whereas both regulatory and catalytic domains of PKC-
 epsilon contribute to in vitro transformation.";
 RT Oncogene 16:53-60(1998).
 RL [3]
 RN NUCLEOTIDE SEQUENCE.
 RP TISSUE=Brain;
 RA Wheeler D.L.;
 RT Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: This is calcium-independent, phospholipid-dependent,
 CC serine- and threonine-specific enzyme.
 CC -1- FUNCTION: PKC is activated by diacylglycerol which in turn
 CC phosphorylates a range of cellular proteins. PKC also serves as
 CC the receptor for phorbol esters, a class of tumor promoters.
 CC -1- PM: Phosphorylation on Thr-566 triggers autophosphorylation on
 CC Ser-729 (By similarity).
 CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family. PKC
 CC subfamily.
 CC -1- SIMILARITY: Contains 2 phorbol-ester/DAG-type zinc fingers.
 CC -----
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use as long as its content is in no way modified and this statement is not
 CC removed.
 CC -----
 DR EMBL; AF028009; AAB84189.1; -; mRNA.
 DR EMBL; AF325507; AAG3692.1; -; mRNA.
 DR PIR; S02270; KIMSC.
 DR HSSP; P09216; 1GMI.
 DR SMR; P16054; 1-136.
 DR IntAct; P16054; -.
 DR Ensemble; ENSMUSG00000055637; Mus musculus.
 DR MGI; MGI:97599; Pkce.
 DR GO; GO:0005737; C:cytoplasm; IDA.
 DR GO; GO:0005634; C:nucleus; IDA.
 DR GO; GO:0004699; F:calcium-independent protein kinase C activity; IDA.
 DR GO; GO:0007655; P:chemosensory behavior; TAS.
 DR GO; GO:0006468; P:protein amino acid phosphorylation; IDA.
 DR GO; GO:0050730; P:regulation of peptidyl-tyrosine phosphoryla. . .; IMP.
 DR InterPro; IPR000008; C2.
 DR InterPro; IPR002219; DAG_Pe_bd.
 DR InterPro; IPR000961; Kinase_C.
 DR InterPro; IPR000719; Prot_kinase.
 DR InterPro; IPR008271; Ser_thr_pkin_AS.
 DR InterPro; IPR002290; Ser_thr_pkinase.

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DR Pfam; PF00130; Cl 1; 2.
DR Pfam; PF00168; C2; 1.
DR Pfam; PF00069; Kinase; 1.
DR Pfam; PF00433; Kinase; C; 1.
DR PRINTS; PR00360; C2DOMAIN.
DR PRINTS; PR00008; DAGPDOMAIN.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00109; C1; 2.
DR SMART; SM00239; C2; 1.
DR SMART; SM00133; S_TK_X; 1.
DR SMART; SM00220; S_TK; 1.
DR PROSITE; PS50004; C2 DOMAIN; 1.
DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
DR PROSITE; PS50011; PROTEIN KINASE DOM; 1.
DR PROSITE; PS00108; PROTEIN KINASE ST; 1.
DR PROSITE; PS00479; ZF_DAG_PE_1; 2.
DR PROSITE; PS50081; ZF_DAG_PE_2; 2.
DR ATP-binding; Kinase; Metal-binding; Nucleotide-binding;
KW Serine/threonine-protein kinase; Phosphorylation; Repeat;
KM Serine/threonine-protein kinase; Transferase; Zinc; Zinc-finger.
FT DOMAIN 1 99
FT ZN_FING 408 668 Protein kinase.
FT ZN_FING 169 220 Phorbol-ester/DAG-type 1.
FT ZN_FING 242 292 Phorbol-ester/DAG-type 2.
FT NP_BIND 414 422 ATP (By similarity).
FT ACT_SITE 532 532 Proton acceptor (By similarity).
FT BINDING 437 437 ATP (By similarity).
FT MOD_RES 566 566 Phosphothreonine (By similarity).
FT MOD_RES 703 703 Phosphothreonine (by autocatalysis)
(Potential).
FT MOD_RES 710 710 Phosphothreonine (by autocatalysis)
(Potential).
FT MOD_RES 729 729 Phosphoserine (by autocatalysis) (By
similarity).
FT SEQUENCE 737 AA; 83561 MW; 7AEBBCC10C99F57 CRC64;
SQ
Query Match 100.0%; Score 48; DB 1; Length 737;
Best Local Similarity 100.0%; Pred. No. 0.6;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 HDAPIGYD 8
Db 85 HDAPIGYD 92

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RL FEBS Lett. 226:125-128(1987).
CC -1- FUNCTION: This is calcium-independent, phospholipid-dependent,
CC serine- and threonine-specific enzyme.
CC -1- FUNCTION: PKC is activated by diacylglycerol which in turn
CC phosphorylates a range of cellular proteins. PKC also serves as
CC the receptor for phorbol esters, a class of tumor promoters.
CC -1- PFM: Phosphorylation on Thr-566 triggers autophosphorylation on
CC Ser-729 (By similarity).
CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family. PKC
CC subfamily.
CC -1- SIMILARITY: Contains 1 C2 domain.
CC -1- SIMILARITY: Contains 2 phorbol-ester/DAG-type zinc fingers.
CC -----
CC This Swiss-Prot entry is copyrighted. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR EMBL; M18331; AAA41872.1; -; mRNA.
DR PIR; B28163; KIRPCE.
DR PDB; 1GMT; X-ray; A=1-136.
DR RGD; 61925; PKce.
DR GO; GO:0007242; P:intracellular signaling cascade; IDA.
DR InterPro; IPR000008; C2.
DR InterPro; IPR002219; DAG_PE_bd.
DR InterPro; IPR000961; PKinase_C.
DR InterPro; IPR007719; Prot_Kinase.
DR InterPro; IPR008271; Ser_thr_pkin_AS.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR Pfam; PF00130; Cl 1; 2.
DR Pfam; PF00168; C2; 1.
DR Pfam; PF00069; Kinase; 1.
DR Pfam; PF00433; Kinase; C; 1.
DR PRINTS; PR00360; C2DOMAIN.
DR PRINTS; PR00008; DAGPDOMAIN.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00109; C1; 2.
DR SMART; SM00239; C2; 1.
DR SMART; SM00133; S_TK_X; 1.
DR SMART; SM00220; S_TK; 1.
DR PROSITE; PS50004; C2 DOMAIN; 1.
DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
DR PROSITE; PS50011; PROTEIN KINASE DOM; 1.
DR PROSITE; PS00108; PROTEIN KINASE ST; 1.
DR PROSITE; PS00479; ZF_DAG_PE_1; 2.
DR PROSITE; PS50081; ZF_DAG_PE_2; 2.
DR 3D-structure; ATP-binding; Kinase; Metal-binding; Nucleotide-binding;
KW Phorbol-ester binding; Phosphorylation; Repeat;
KM Serine/threonine-protein kinase; Transferase; Zinc; Zinc-finger.
FT DOMAIN 1 99
FT ZN_FING 169 220 Protein kinase.
FT ZN_FING 242 292 Phorbol-ester/DAG-type 1.
FT NP_BIND 414 422 ATP (By similarity).
FT ACT_SITE 532 532 Proton acceptor (By similarity).
FT BINDING 437 437 ATP (By similarity).
FT MOD_RES 566 566 Phosphothreonine (By similarity).
FT MOD_RES 703 703 Phosphothreonine (by autocatalysis)
(Potential).
FT MOD_RES 710 710 Phosphothreonine (by autocatalysis)
(Potential).
FT MOD_RES 729 729 Phosphoserine (by autocatalysis) (By
similarity).
FT STRAND 2 16
FT HELIX 4 25
FT STRAND 40 46
FT TURN 47 48
FT STRAND 49 53
FT STRAND 64 76
FT STRAND 78 85
FT STRAND 93 101
FT HELIX 102 105

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FT TURN 106 106
FT TURN 108 109
FT STRAND 112 118
FT STRAND 120 120
FT STRAND 124 135
SQ SEQUENCE 737 AA; 83478 MW; 6AD6999EFD2659F CRC64;

Query Match
Query Similarity 100.0%; Score 48; DB 1; Length 737;
Best Local 100.0%; Pred. No. 0.6;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 HDAPICVD 8
Db 85 HDAPICVD 92

RESULT 6
O6DVL1_RAT PRELIMINARY; PRT; 737 AA.
ID O6DVL1_RAT PRELIMINARY; PRT; 737 AA.
AC O6DVL1;
DT 25-OCT-2004 (TREMBlrel. 28, Created)
DT 25-OCT-2004 (TREMBlrel. 28, Last sequence update)
DT 25-OCT-2004 (TREMBlrel. 28, Last annotation update)
DE Protein kinase C epsilon.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridea; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RC NUCLEOTIDE SEQUENCE.
RA STRAIN=Mistar; TISSUE=Liver;
RA Buchfield J.G., Schmitz-Peiffer C., Biden T.J.;
RA Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.
RL -1- FUNCTION: PKC is activated by diacylglycerol which in turn
phosphorylates a range of cellular proteins. PKC also serves as
the receptor for phorbol esters, a class of tumor promoters (By
similarity).
CC -1- FUNCTION: This is a calcium-activated, phospholipid-dependent,
serine- and threonine-specific enzyme (By similarity).
CC -1- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC -1- COFACTOR: Binds 3 calcium ions per subunit. The ions are bound to
the C2 domain (By similarity).
CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
CC -1- SIMILARITY: Contains 1 C2 domain.
DR EMBL; AY642593; AAF5503.1; -; mRNA.
DR SMR; O6DVL1; 1-136.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR GO; GO:0007242; P:intracellular signaling cascade; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR000008; C2.
DR InterPro; IPR002219; DAG_Pe_bd.
DR InterPro; IPR000961; PKinase_C.
DR InterPro; IPR000719; Prot_Kinase.
DR InterPro; IPR008271; Ser_Thr_Pkin_AS.
DR InterPro; IPR002290; Ser_Thr_Pkinase.
DR InterPro; IPR001245; Tyr_Pkinase.
DR Pfam; PF00130; C1_1; 2.
DR Pfam; PF00168; C2_1.
DR Pfam; PF00069; PKinase; 1.
DR Pfam; PF00433; PKinase_C; 1.
DR PRINTS; PR00360; C2DOMAIN.
DR PRINTS; PR00008; DAGPEDOMAIN.
DR ProDom; PD000001; Prot_Kinase; 1.
DR SMART; SM00109; C1; 2.
DR SMART; SM00239; C2; 1.
DR SMART; SM00133; S_TK_X; 1.
DR SMART; SM00220; S_TKc; 1.
DR SMART; SM00219; TyrKc; 1.
DR PROSITE; PS50004; C2_DOMAIN; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
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DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
DR PROSITE; PS00479; ZF_DAG_Pe_1; 2.
DR PROSITE; PS50081; ZF_DAG_Pe_2; 2.
DR ATP-binding; Calcium_Kinase; Nucleotide-binding;
KW Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 737 AA; 83576 MW; CF77776819A26333 CRC64;

Query Match
Query Similarity 100.0%; Score 48; DB 2; Length 737;
Best Local 100.0%; Pred. No. 0.6;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 HDAPICVD 8
Db 85 HDAPICVD 92

RESULT 7
Q4SG88_TETNG PRELIMINARY; PRT; 754 AA.
ID Q4SG88_TETNG PRELIMINARY; PRT; 754 AA.
AC Q4SG88;
DT 13-SEP-2005 (TREMBlrel. 31, Created)
DT 13-SEP-2005 (TREMBlrel. 31, Last sequence update)
DT 13-SEP-2005 (TREMBlrel. 31, Last annotation update)
DE Chromosome 17 SCAP14597, whole genome shotgun sequence.
DE (Fragment).
GN ORFNames=STENG00018762001;
OS Tetraodon nigroviridis (Green puffer).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorphi; Acanthopterygii; Percomorphi; Tetraodontiformes;
OC Tetraodontidae; Tetraodon.
OX NCBI_TaxID=99883;
RN [1]
RC NUCLEOTIDE SEQUENCE.
RA Tallon O., Aury J.M., Brunet F., Petit J.L., Stange-Thomann N.,
RA Mancel E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,
RA Nicaud S., Jaffe D., Fisher S., Litalien G., Dossat C., Segurens B.,
RA Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,
RA Anthouard V., Jabin C., Castelli V., Katinka M., Vacherie B.,
RA Bismont C., Skalli Z., Cattolico L., Poulsen J., De Bernardis V.,
RA Criand C., Duprat S., Broctier P., Couranceau J.P., Gouy J.,
RA Patra G., Lardier G., Chapple C., McKernan K.J., McEwan P., Bosak S.,
RA Kellis M., Volff J.N., Guigo R., Zody M.C., Mesirov J.,
RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
RA Landel V., Schachter V., Quetier F., Saurin W., Scarpelli C.,
RA Winkler P., Lander B.S., Weissenbach J., Roest Crolius H.;
RA "Genome duplication in the teleost fish Tetraodon nigroviridis reveals
RT the early vertebrate proto-karyotype.";
RL Nature 431:946-957(2004).
RN [2]
RC NUCLEOTIDE SEQUENCE.
RA Genoscope; Whitehead Institute Centre for Genome Research;
RA Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
RL -1- CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
preliminary data.
CC -1- FUNCTION: Plays a key role in the control of the eukaryotic cell
cycle. It is required in higher cells for entry into S-phase and
mitosis. Component of the kinase complex that phosphorylates the
repetitive C-terminus of RNA polymerase II. Catalytic component of
MPP (By similarity).
CC -1- SUBUNIT: Forms a stable but non-covalent complex with cyclin B in
mature oocytes (By similarity).
CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
CC -1- SIMILARITY: Contains 1 C2 domain.
DR EMBL; CA501014597; CAG00344.1; -; Genomic_DNA.
DR InterPro; IPR000008; C2.
DR InterPro; IPR002219; DAG_Pe_bd.
DR InterPro; IPR000961; PKinase_C.
DR InterPro; IPR000719; Prot_Kinase.
DR InterPro; IPR008271; Ser_Thr_Pkin_AS.
DR InterPro; IPR002290; Ser_Thr_Pkinase.
```

```
DR InterPro; IPR001245; Tyr_kinase.
DR Pfam; PF00130; C1.1; 2.
DR Pfam; PF00168; C2; 1.
DR Pfam; PF00069; Pkinase_C; 1.
DR PRINTS; PR00008; DAGPEDOMAIN.
DR PRODOM; PD000001; Prot_kinase; 1.
DR SMART; SM00109; C1; 2.
DR SMART; SM00239; C2; 1.
DR SMART; SM00133; S_TK_X; 1.
DR SMART; SM00220; S_TKC; 1.
DR SMART; SM00219; TYKc; 1.
DR PROSITE; PS50004; C2 DOMAIN; 1.
DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
DR PROSITE; PS50011; PROTEIN KINASE DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
DR PROSITE; PS00479; ZF_DAG_PE_1; 2.
DR PROSITE; PS50081; ZF_DAG_PE_2; 2.
DR ATP-binding; Kinase; Nucleotide-binding;
KW Serine/threonine-protein kinase; Transferase.
FT NON TER 754 754
SQ SEQUENCE 754 AA; 85146 MW; F9C3DA77EB84DF7 CRC64;

Query Match 100.0%; Score 48; DB 2; Length 754;
Best Local Similarity 100.0%; Pred. No. 0.61;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 HDAPIGYD 8
DB 72 HDAPIGYD 79

RESULT 8
Q4T021.TETNG PRELIMINARY; PRT; 895 AA.
ID Q4T021;
AC Q4T021;
DT 13-SEP-2005 (TREMBlrel. 31, Created)
DT 13-SEP-2005 (TREMBlrel. 31, Last sequence update)
DE Chromosome undetermined SCF11390, whole genome shotgun sequence.
DE (Fragment).
GN ORFNames=GSTENG0009554001;
OS Tetradon nigroviridis (Green puffer).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC Tetraodontidae; Tetraodon.
OX NCBI_TaxID=99883;
RN [1];
RP NUCLEOTIDE SEQUENCE.
RA Jallion O., Aury J.M., Brunet F., Petit J.L., Stange-Thomann N.,
RA Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,
RA Micard S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,
RA Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,
RA Anthouard V., Jubin C., Castelli V., Katinka M., Vacherie B.,
RA Blomont C., Skalli Z., Catalicio L., Poulain J., De Berardinis V.,
RA Ctraud C., Duprat S., Broctier P., Coutanceau J.P., Gouzy J.,
RA Parra G., Lardier G., Chapple C., McKernan K.J., McEwan P., Bosak S.,
RA Kellis M., Wolff J.N., Guigo R., Zody M.C., Mesirov J.,
RA Landrad-Toh K., Bitren B., Nishbaum C., Kahn D., Robinson-Rechavi M.,
RA Lander V., Schachter V., Quetier F., Saurin W., Scarpelli C.,
RA Wincker P., Lander E.S., Weissenbach J., Roest Crolius H.,
RT "Genome duplication in the teleost fish Tetraodon nigroviridis reveals
the early vertebrate proto-karyotype.";
RL Nature 431:946-957(2004).
RN [2];
RP NUCLEOTIDE SEQUENCE.
RG Genoscope; Whitehead Institute Centre for Genome Research;
RL Submitted (FEB-2004) to the EMBL/Genbank/DBJ databases.
CC -1- CAUTION: The sequence shown here is derived from an
CC EMBL/Genbank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
CC -1- FUNCTION: Plays a key role in the control of the eukaryotic cell
```

```
CC cycle. It is required in higher cells for entry into S-phase and
CC mitosis. Component of the kinase complex that phosphorylates the
CC repetitive C-terminus of RNA polymerase II. Catalytic component of
CC MPF (By similarity).
CC -1- FUNCTION: This is a calcium-activated, phospholipid-dependent,
CC serine- and threonine-specific enzyme (By similarity).
CC -1- COFACTOR: Binds 3 calcium ions per subunit. The ions are bound to
CC the C2 domain (By similarity).
CC -1- SUBUNIT: Forms a stable but non-covalent complex with cyclin B in
CC mature oocytes (By similarity).
CC -1- SIMILARITY: Contains 1 C2 domain.
CC EMBL; CAAB01011390; CAP93761.1; -; Genomic_DNA.
DR InterPro; IPR000008; C2.
DR InterPro; IPR002219; DAG_PE_bd.
DR InterPro; IPR000961; Pkinase_C.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR008271; Ser_Thr_kin_AS.
DR InterPro; IPR002290; Ser_Thr_kinase.
DR InterPro; IPR001245; Tyr_kinase.
DR Pfam; PF00130; C1.1; 2.
DR Pfam; PF00168; C2; 1.
DR Pfam; PF00069; Pkinase; 1.
DR PRINTS; PR00360; C2DOMAIN.
DR PRINTS; PR00008; DAGPEDOMAIN.
DR PRODOM; PD000001; Prot_kinase; 1.
DR SMART; SM00109; C1; 2.
DR SMART; SM00239; C2; 1.
DR SMART; SM00133; S_TK_X; 1.
DR SMART; SM00220; S_TKC; 1.
DR SMART; SM00219; TYKc; 1.
DR PROSITE; PS50004; C2 DOMAIN; 1.
DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
DR PROSITE; PS00479; ZF_DAG_PE_1; 1.
DR PROSITE; PS50081; ZF_DAG_PE_2; 2.
DR ATP-binding; Kinase; Nucleotide-binding;
KW Serine/threonine-protein kinase; Transferase.
FT NON TER 895 895
SQ SEQUENCE 895 AA; 99736 MW; 09C6846992500B55 CRC64;

Query Match 100.0%; Score 48; DB 2; Length 895;
Best Local Similarity 100.0%; Pred. No. 0.73;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 HDAPIGYD 8
DB 84 HDAPIGYD 91

RESULT 9
Q4T025.TETNG PRELIMINARY; PRT; 118 AA.
ID Q4T025;
AC Q4T025;
DT 13-SEP-2005 (TREMBlrel. 31, Created)
DT 13-SEP-2005 (TREMBlrel. 31, Last sequence update)
DE Chromosome undetermined SCAP4616, whole genome shotgun sequence.
DE (Fragment).
GN ORFNames=GSTENG0001687001;
OS Tetradon nigroviridis (Green puffer).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC Tetraodontidae; Tetraodon.
OX NCBI_TaxID=99883;
RN [1];
RP NUCLEOTIDE SEQUENCE.
RA Jallion O., Aury J.M., Brunet F., Petit J.L., Stange-Thomann N.,
RA Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,
RA Micard S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,
RA Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,
RA Anthouard V., Jubin C., Castelli V., Katinka M., Vacherie B.,
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RA Blomont C., Skalli Z., Catolico L., Poulain J., De Bernardis V.,
 RA Crnaud C., Duprat S., Broctier P., Coutanceau J.P., Gouy J.,
 RA Parra G., Lardier G., Chapple C., McKernan K.J., McEwan P., Bosak S.,
 RA Kallis M., Volff J.N., Guigo R., Zody M.C., Mestrov J.,
 RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
 RA Lander V., Schachter V., Queller F., Saurin W., Scarpetti C.,
 RA Wincker P., Lander E.S., Weissbach J., Roest Crolius H.,
 RT "Genome duplication in the teleost fish Tetraodon nigroviridis reveals
 RT the early vertebrate proto-karyotype.";
 RL Nature 431:946-957(2004).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RG Genoscope; Whitehead Institute Centre for Genome Research;
 RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
 CC -1- CAUTION: The sequence shown here is derived from an
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.
 CC -1- SIMILARITY: Contains 1 C2 domain.
 CC EMBL; CAAB01004616; CAF88387.1; -; Genomic_DNA.
 DR InterPro; IPR000008; C2.
 DR Pfam; PF00168; C2; 1.
 DR PRINTS; PR00360; C2DOMAIN.
 DR SMART; SM02239; C2; 1.
 DR PROSITE; PS50004; C2_DOMAIN; 1.
 FT NON TER 118
 SQ SEQUENCE 118 AA; 13444 MM; 950C9A4F27B7E08C CRC64;
 QY 1 HDAPIGYD 8
 Db 84 HDTPIGYD 91
 Query Match 91.7%; Score 44; DB 2; Length 118;
 Best Local Similarity 87.5%; Pred. No. 0.58;
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

RESULT 10
 Q4RM42.TETNG PRELIMINARY; PRT; 766 AA.
 AC Q4RM42;
 DT 13-SEP-2005 (TREMBlrel. 31, Created)
 DT 13-SEP-2005 (TREMBlrel. 31, Last sequence update)
 DT 13-SEP-2005 (TREMBlrel. 31, Last annotation update)
 DB Chromosome 10 SCAF15019, whole genome shotgun sequence.
 DE (Fragment).
 GN ORFNames=GSTENG00032218001;
 OS Tetraodon nigroviridis (Green puffer).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 OC Acanthomorphi; Acanthopterygii; Percomorphi; Tetraodontiformes;
 OC Tetraodontidae; Tetraodontidae; Tetraodon.
 OX NCBI_TaxID=99983;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Jallion O., Aury J.M., Brunet F., Petit J.L., Stange-Thomann N.,
 RA Mauceli E., Bounaou L., Fischer C., Ozou-Costaz C., Bernot A.,
 RA Nicoud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,
 RA Dastiv C., Salanoubat M., Levy M., Boudet N., Casatelli S.,
 RA Anthonard V., Rubin C., Casatelli V., Katinka M., Vacherie B.,
 RA Blomont C., Skalli Z., Catolico L., Poulain J., De Bernardis V.,
 RA Crnaud C., Duprat S., Broctier P., Coutanceau J.P., Guzy J.,
 RA Parra G., Lardier G., Chapple C., McKernan K.J., McEwan P., Bosak S.,
 RA Kallis M., Volff J.N., Guigo R., Zody M.C., Mestrov J.,
 RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
 RA Lander V., Schachter V., Queller F., Saurin W., Scarpetti C.,
 RA Wincker P., Lander E.S., Weissbach J., Roest Crolius H.,
 RT "Genome duplication in the teleost fish Tetraodon nigroviridis reveals
 RT the early vertebrate proto-karyotype.";
 RL Nature 431:946-957(2004).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RG Genoscope; Whitehead Institute Centre for Genome Research;
 RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.

CC -1- CAUTION: The sequence shown here is derived from an
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.
 CC -1- FUNCTION: Plays a key role in the control of the eukaryotic cell
 CC cycle. It is required in higher cells for entry into S-phase and
 CC mitosis. Component of the kinase complex that phosphorylates the
 CC repetitive C-terminus of RNA polymerase II. Catalytic component of
 CC MPF (By similarity).
 CC -1- FUNCTION: This is a calcium-activated, phospholipid-dependent,
 CC serine- and threonine-specific enzyme (By similarity).
 CC -1- COFACTOR: Binds 3 calcium ions per subunit. The ions are bound to
 CC the C2 domain (By similarity).
 CC -1- SUBUNIT: Forms a stable but non-covalent complex with cyclin B in
 CC mature oocytes (By similarity).
 CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
 CC EMBL; CAAB01015019; CAG10540.1; -; Genomic_DNA.
 DR InterPro; IPR000008; C2.
 DR InterPro; IPR002219; DAG_PE_bd.
 DR InterPro; IPR000961; Pkinase_C.
 DR InterPro; IPR000719; Prot_kinase.
 DR InterPro; IPR008271; Ser_Thr_pkin_AS.
 DR InterPro; IPR002290; Ser_Thr_pkinase.
 DR Pfam; PF001245; Tyr_Pkinase.
 DR Pfam; PF00130; C1_1; 1.
 DR Pfam; PF00168; C2; 1.
 DR Pfam; PF00069; Pkinase; 1.
 DR Pfam; PF00433; Pkinase_C; 1.
 DR PRINTS; PR00360; C2DOMAIN.
 DR PRINTS; PR00008; DAGREDOMAIN.
 DR ProDom; PD000001; Prot_Kinase; 1.
 DR SMART; SM00109; C1; 1.
 DR SMART; SM00239; C2; 1.
 DR SMART; SM00133; S_TK_X; 1.
 DR SMART; SM00220; S_TKC; 1.
 DR SMART; SM00219; TYR_KC; 1.
 DR PROSITE; PS50004; C2_DOMAIN; 1.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
 DR PROSITE; PS00479; ZF_DAG_PE_1; 1.
 DR PROSITE; PS50081; ZF_DAG_PE_2; 1.
 DR ATP-binding; Kinase; Nucleotide-binding;
 KW Serine/threonine-protein kinase; Transferase.
 FT NON TER 766
 SQ SEQUENCE 766 AA; 85776 MM; 588A7229B2AED5AA CRC64;
 QY 1 HDAPIGYD 8
 Db 84 HDTPIGYD 91
 Query Match 91.7%; Score 44; DB 2; Length 766;
 Best Local Similarity 87.5%; Pred. No. 4.3;
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

RESULT 11
 Q8D965.VIBVU PRELIMINARY; PRT; 774 AA.
 AC Q8D965;
 DT 01-MAR-2003 (TREMBlrel. 23, Created)
 DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
 DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
 DE P pilus assembly protein.
 GN OrderedLocNames=VV12741;
 OS Vibrio vulnificus.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
 OC Vibrionaceae; Vibrrio.
 OX NCBI_TaxID=672;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=CMCP6;
 RA Rhee J.H., Kim S.Y., Chung S.S., Kim J.U., Moon Y.H., Jeong H.,

RA Choy H.E.;
 RT "Complete genome sequence of *Vibrio vulnificus* CMCP6.";
 RL Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AE016806; AA011085.1; -, Genomic_DNA.
 DR InterPro; IPR002086; Aldenhyd_dehydrotrog.
 DR InterPro; IPR000194; ATPase_a/bcentre.
 DR PROSITE; PS00687; ALDEHYDE DEHYDR GLU; UNKNOWN_1.
 DR PROSITE; PS00152; ATPASE_ALPHA_BETA; UNKNOWN_1.
 KM Complete proteome.
 SQ SEQUENCE 774 AA; 86708 MW; C68AAB58F29F6924 CRC64;

Query Match 85.4%; Score 41; DB 2; Length 774;
 Best Local Similarity 75.0%; Pred. No. 19;
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HDAPICD 8
 Db 654 HNAFLGYD 661

RESULT 12
 07MLA7_VIBVY
 ID 07MLA7_VIBVY PRELIMINARY; PRT; 800 AA.
 AC 07MLA7;
 DT 01-MAR-2004 (TREMBlrel. 26, Created)
 DT 01-MAR-2004 (TREMBlrel. 26, Last sequence update)
 DE 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
 DE P plus assembly protein, porin PapC.
 GN OrderedLocustNames=VVI520;
 OS *Vibrio vulnificus* (strain VJ016).
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
 OC Vibrionaceae; *Vibrio*.
 OX NCBI_TaxID=196600;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX PubMed=14656965; DOI=10.1101/gr.1295503;
 RA Chen C.-Y., Wu K.-M., Chang Y.-C., Chang C.-H., Tsai H.-C.,
 RA Liao T.-L., Liu Y.-M., Chen H.-J., Shen A.B.-T., Li J.-C., Su T.-L.,
 RA Shao C.-P., Lee C.-T., Hor L.-I., Tsai S.-P.;
 RT "Comparative genome analysis of *Vibrio vulnificus*, a marine
 RT pathogen.";
 RL Genome Res. 13:2577-2587(2003).
 DR EMBL; BA0016021; C: integral to membrane; IEA.
 DR GO; GO:00016021; C: integral to membrane; IEA.
 DR GO; GO:0019867; C: outer membrane; IEA.
 DR GO; GO:0015288; F: porin activity; IEA.
 DR InterPro; IPR002086; Aldenhyd_dehydrotrog.
 DR InterPro; IPR000194; ATPase_a/bcentre.
 DR PROSITE; PS00687; ALDEHYDE DEHYDR GLU; UNKNOWN_1.
 DR PROSITE; PS00152; ATPASE_ALPHA_BETA; UNKNOWN_1.
 KM Complete proteome; Porin.
 SQ SEQUENCE 800 AA; 90024 MW; 499957F81CC88773 CRC64;

Query Match 85.4%; Score 41; DB 2; Length 800;
 Best Local Similarity 75.0%; Pred. No. 19;
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HDAPICD 8
 Db 680 HNAFLGYD 687

RESULT 13
 06GNZ7_XENLA
 ID 06GNZ7_XENLA PRELIMINARY; PRT; 687 AA.
 AC 06GNZ7;
 DT 05-JUL-2004 (TREMBlrel. 27, Created)
 DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
 DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
 MG80770 protein.
 GN Name=MG80770;
 OS *Xenopus laevis* (African clawed frog).
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
 OC Xenopodinae; *Xenopus*; *Xenopus*.
 OX NCBI_TaxID=8355;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Sp1en;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner K.H., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusik K., Farmer A.A., Rubin G.M., Hong L.,
 RA Sapetenko M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Uudin T.B., Toohyuk S., Carninci P., Prange C.,
 RA Raba S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Boak S.A., McKean P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.D., Huiyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz U., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalek U., Smalins D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Sp1en;
 RX MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
 RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
 RA Richardson P.;
 RT "Genetic and genomic tools for *Xenopus* research: The NIH *Xenopus*
 RT initiative.";
 RL Dev. Dyn. 225:384-391(2002).
 RN [3]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Sp1en;
 RX Klein S., Gerhard D.S.;
 RL EMBL; BC073353; AAH73353.1; -, mRNA.
 DR GO; GO:0005524; F: ATP binding; IEA.
 DR GO; GO:0004674; F: protein serine/threonine kinase activity; IEA.
 DR GO; GO:0004713; F: protein-tyrosine kinase activity; IEA.
 DR GO; GO:0007242; P: intracellular signaling cascade; IEA.
 DR GO; GO:0006468; P: protein amino acid phosphorylation; IEA.
 DR InterPro; IPR000008; C2.
 DR InterPro; IPR002219; DAG_Pe-bind.
 DR InterPro; IPR000961; Pkinase C.
 DR InterPro; IPR000719; Pkinase C.
 DR InterPro; IPR008271; Ser_thr_pkin_AS.
 DR InterPro; IPR002290; Ser_thr_pkinase.
 DR InterPro; IPR001245; Tyr_pkinase.
 DR Pfam; PF00130; C1.1; 2.
 DR Pfam; PF00168; C2.1.
 DR Pfam; PF00069; Pkinase.1.
 DR Pfam; PF00433; Pkinase C.1.
 DR PRINTS; PR00360; C2DOMAIN.
 DR PRINTS; PR00008; DAGPEOMAIN.
 DR PRODOM; PD000001; Prot_kinase; 1.
 DR SMART; SM00109; C1.2.
 DR SMART; SM00239; C2.1.
 DR SMART; SM00133; S_TK_X.1.
 DR SMART; SM00220; S_TKc.1.
 DR SMART; SM00219; TYRKC.1.
 DR PROSITE; PSS0004; C2 DOMAIN 2; 1.
 DR PROSITE; PSS00479; DAG_Pe BIND DOM 1; 2.
 DR PROSITE; PSS00081; DAG_Pe BIND DOM 2; 2.
 DR PROSITE; PSS00107; PROTEIN_KINASE_ATP.1.
 DR PROSITE; PSS00011; PROTEIN_KINASE_DOM.1.
 DR PROSITE; PS00108; PROTEIN_KINASE_ST.1.
 SQ SEQUENCE 687 AA; 78400 MW; 6EF3B8D7E1AB6958 CRC64;

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Query Match      83.3%; Score 40; DB 2; Length 687;
Best Local Similarity 75.0%; Pred. No. 27;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 HDAPICVD 8
Db 83 HEPICVD 90

RESULT 14
06N9D6 RHOPA PRELIMINARY; PRT; 421 AA.
ID 06N9D6 RHOPA PRELIMINARY; PRT; 421 AA.
AC 06N9D6;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DE 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE Putative cytochrome P-450 (EC 1.14.-.-).
GN Rhodospseudomonas palustris.
OS Rhodospseudomonas palustris.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Bradyrhizobiaceae; Rhodospseudomonas.
OX NCBI_TaxID=1076;
RX [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=CGA009 / ATCC BAA-98;
RC PubMed=14704707; DOI=10.1038/nbt923;
RA Lamer F. W., Chain P., Hauser L., Lamerdin J. E., Malfatti S., Do L.,
RA Land M. L., Pelletier D. A., Beatty J. T., Lang A. S., Tabita F. R.,
RA Gibson J. L., Hanson T. E., Bobet C., Torres y Torres J. L., Peres C.,
RA Harrison F. H., Gibson J., Harwood C. S.,
RT "Complete genome sequence of the metabolically versatile
RT photosynthetic bacterium Rhodospseudomonas palustris.";
RL Nat. Biotechnol. 22:55-61(2004).
CC -1. SIMILARITY: Belongs to the cytochrome P450 family.
DR EMBL; BX572558; CAE27054.1; -; Genomic DNA.
DR GO; GO:0046872; F:metal ion binding; IEA.
DR GO; GO:0004497; F:monooxygenase activity; IEA.
DR GO; GO:0006118; P:electron transport; IEA.
DR InterPro; IPR002397; BP450.
DR InterPro; IPR001128; Cytochrome_P450.
DR Pfam; PF00067; P450; 1.
DR PRINTS; PR00359; BP450.
DR PRINTS; PR00385; P450.
DR PROSITE; PS00086; CYTOCHROME_P450; UNKNOWN 1.
KM Complete proteome; Heme; Iron; Metal-binding; Monooxygenase;
KW Oxidoreductase.
SQ SEQUENCE 421 AA; 48554 MW; A10F3A5302DAD22F CRC64;

Query Match      81.2%; Score 39; DB 2; Length 421;
Best Local Similarity 85.7%; Pred. No. 26;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 DAPICVD 8
Db 97 DAPICVD 103

RESULT 15
08H055 ORYZA PRELIMINARY; PRT; 586 AA.
ID 08H055 ORYZA PRELIMINARY; PRT; 586 AA.
AC 08H055;
DT 01-MAR-2003 (TREMBlrel. 23, Created)
DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE Putative DHC-type zinc finger protein.
GN Name=OSUNBA0014006.17;
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaceae; Oryza.
OX NCBI_TaxID=39947;
RX [1]

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RP NUCLEOTIDE SEQUENCE.
RA Wang R. A., Yu Y., Soderlund C., Kim H.-R., Rambo T., Saeki C.,
RA Currie J., Collura K.,
RL Submitted (JEC-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; ACJ05928; AAN77310.1; -; Genomic DNA.
DR Gramene; Q8H055;
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR GO; GO:0046872; F:metal ion binding; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR001594; ZnF_DHHC.
DR Pfam; PF01529; zf-DHHC; 1.
DR ProDom; PD003041; ZnF_DHHC; 1.
DR PROSITE; PS50216; ZF_DHHC; 1.
SQ SEQUENCE 586 AA; 64254 MW; 2AFAF2B8A3E1F3A CRC64;

Query Match      81.2%; Score 39; DB 2; Length 586;
Best Local Similarity 75.0%; Pred. No. 36;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 HDAPICVD 8
Db 408 HDVPIGHD 415

RESULT 16
060070 SCHPO PRELIMINARY; PRT; 652 AA.
ID 060070 SCHPO PRELIMINARY; PRT; 652 AA.
AC 060070;
DT 01-AUG-1998 (TREMBlrel. 07, Created)
DT 01-AUG-1998 (TREMBlrel. 07, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE SPIC13G1.08c protein (Ash2 protein).
GN Name=ash2; ORFNames=SPIC13G1.08c;
OS Schizosaccharomyces pombe (fission yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC Schizosaccharomycetaceae; Schizosaccharomycetaceae;
OC NCBI_TaxID=4896;
RX [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=972;
RC MEDLINE=21849401; PubMed=11859360; DOI=10.1038/nature724;
RC Wood V., Gwilliam R., Rajandream M. A., Lyne M. H., Lyne R., Stewart A.,
RA Sgouros J. G., Peat N., Hayles J., Baker S. G., Basham D., Bowman S.,
RA Brooks K. D., Brown D., Brown S., Chillingworth T., Churcher C. M.,
RA Collins M., Connor R., Cronin A., Davis P., Fellwell T., Fraser A.,
RA Gentles S., Hornby T., Howarth S., Huckle E. J., Hunt S., Jagsi K.,
RA Holroyd S., Hornby T., Howarth S., Huckle E. J., Hunt S., Jagsi K.,
RA James K. D., Jones L., Jones M., Leather S., McDonald S., McLean J.,
RA Mooney P., Moule S., Mungall K. L., Murphy L. D., Niblett D., Odell C.,
RA Oliver K., O'Neill S., Pearson D., Quail M. A., Rabinowitch E.,
RA Rutherford K. M., Rutter S., Saunders D., Seeger K., Sharp S.,
RA Skelton J., Simmonds M. N., Squares R., Squares S., Stevens K.,
RA Taylor K., Taylor R. G., Tiley A., Walsh S. V., Warren T., Whitehead S.,
RA Woodward J. R., Voiclaert G., Aert R., Robben J., Grymoprez B.,
RA Welljens I., Vansteelandt E., Rieger M., Schaefer M., Mueller-Auer S.,
RA Gabel C., Fuchs M., Duesterhoeft A., Fritz C., Holzer E., Moestl D.,
RA Hilbert H., Borzym K., Langer I., Beck A., Lehnach H., Reinhardt R.,
RA Pohl T. M., Beger P., Zimmermann W., Medler H., Mamut R., Purnelle B.,
RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,
RA Galibert F., Aves S. J., Xiang Z., Hunt C., Moore K., Huzar S. M.,
RA Lucas M., Rochet M., Galliard C., Tallada V. A., Garzon A., Thode G.,
RA Dage R. R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
RA Dominguez A., Revuelta J. L., Moreno S., Armstrong J., Forsburg S. L.,
RA Cerutti L., Lowe T., McCombie W. R., Paulsen I., Potashkin J.,
RA Shpakovsky G. V., Useery D., Barrett B. G., Nurse P.,
RT "The genome sequence of Schizosaccharomyces pombe.";
RL Nature 415:871-880(2002).
DR EMBL; AL022600; CAA18661.1; -; Genomic DNA.
DR PIR; T39409; T39409.
DR GeneDB_Spombe; SPIC13G1.08c; -.
DR GO; GO:0048188; C:COMPASS complex; IDA.

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DR GO; GO:0048189; C:lid2 complex; IDA.
 DR InterPro; IPR003877; SPRY receptor.
 DR InterPro; IPR001965; Znf_PHD.
 DR Pfam; PF00622; SPRY.1.
 DR SMART; SM00249; PHD.1.
 DR SMART; SM00449; SPRY.1.
 DR PROSITE; PS01359; ZF_PHD_1; UNKNOWN_1.
 KW Complete proteome.
 SQ SEQUENCE 652 AA; 74252 MW; 998F783EC8BD0360 CRC64;

Query Match 81.2%; Score 39; DB 2; Length 652;
 Best Local Similarity 85.7%; Pred. No. 41;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 2 DAPVGYD 8
 DB 419 DAPVGYD 425

RESULT 17
 08H922 ORYSA PRELIMINARY; PRT; 731 AA.
 AC 08H922;
 DT 01-MAR-2003 (TREMBLrel. 23, Created)
 DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)
 DT 01-FEB-2005 (TREMBLrel. 29, Last annotation update)
 DE Hypothetical protein OSUNBa0071K18.2.
 GN ORFNames=OSUNBa0071K18.2;
 OS Oryza sativa (Japonica cultivar-group).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Eubacteriales; Oryzaceae; Oryza.
 CC NCBI_TaxID=39947;
 RX NCU1_TaxID=39947;

RP NUCLEOTIDE SEQUENCE.
 RA Buell C.R., Yuan Q., Qiyang S., Liu J., Gansberger K., Jones K.M.,
 RA Overton I.L., Teltzin T., Kim M.M., Bera J.J., Jin S.S.,
 RA Fadrosh D.W., Tallon L.J., Koo H., Zismann V., Hsiao J., Blunt S.,
 RA Vanaken S.S., Riedmiller S.B., Utecher T.T., Feldblyum T.V.,
 RA Yang Q.Q., Haas B.U., Suh B.B., Peterson J.J., Quackenbush J.,
 RA White O., Salzberg S.L., Fraser C.M.;
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RA Buell R.;
 RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP NUCLEOTIDE SEQUENCE.
 RA The Rice Chromosome 10 Sequencing Consortium;
 RT "In-depth view of structure, activity, and evolution of rice
 RT chromosome 10";
 RL Science 300:1566-1569 (2003).
 RN [4]
 RP NUCLEOTIDE SEQUENCE.
 RA Buell C.R., Wing R.A., McCombie W.R., Messing J., Yuan Q.;
 RL Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AC027038; AAN05523.1; -; Genomic_DNA.
 DR EMBL; AB017103; AAP54178.1; -; Genomic_DNA.
 DR Gramene; 08H922; -;
 DR GO; GO:0000151; C:ubiquitin ligase complex; IEA.
 DR GO; GO:0004842; F:ubiquitin-protein ligase activity; IEA.
 DR GO; GO:0008270; F:zinc ion binding; IEA.
 DR InterPro; IPR002035; VWF_A.
 DR InterPro; IPR001841; Znf_ring.
 DR Pfam; PF00092; VWA.1.
 DR Pfam; PF00097; zf-C3HC4.1.
 GN PRINTS; PR00453; VWFADOMAIN.
 DR SMART; SM00184; RING.1.
 DR SMART; SM00327; VWA.1.
 DR PROSITE; PS50234; WVFA.1.
 DR PROSITE; PS50089; ZF_RING_2; 1.
 KW Hypothetical protein_

SQ SEQUENCE 731 AA; 78227 MW; 335F9C377831ADU7 CRC64;
 Query Match 81.2%; Score 39; DB 2; Length 731;
 Best Local Similarity 85.7%; Pred. No. 46;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 2 DAPVGYD 8
 DB 553 DAPVGYD 559

RESULT 18
 0550S2 CRYNE PRELIMINARY; PRT; 861 AA.
 AC 0550S2;
 ID 0550S2;
 DT 13-SEP-2005 (TREMBLrel. 31, Created)
 DT 13-SEP-2005 (TREMBLrel. 31, Last sequence update)
 DT 13-SEP-2005 (TREMBLrel. 31, Last annotation update)
 DE Hypothetical protein.
 GN ORFNames=CNBP2660;
 OS Cryptococcus neoformans var. neoformans B-3501A.
 OC Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Heterobasidiomycetes;
 OC Tremellomycetidae; Tremellales; Filobasidiella.
 CC NCBI_TaxID=283643;
 RX NCU1_TaxID=283643;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=B-3501A;
 RA Fung E., Hyman R.W., Rowley D., Bruno D., Miranda M., Fukushima M.,
 RA Wicks B.L., Fu J., Davis R.W.;
 RT "Cryptococcus neoformans serotype D sequencing."
 RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
 CC -!- CAUTION: The sequence shown here is derived from an
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.
 DR EMBL; AAEY0100032; EAL19939.1; -; Genomic_DNA.
 DR InterPro; IPR001810; F-box.
 DR InterPro; IPR001680; WD40.
 DR Pfam; PF00646; F-box; 1.
 DR Pfam; PF00400; WD40; 7.
 DR PRINTS; PR00320; GPROTEINRPT.
 DR PRODOM; PD000018; WD40; 2.
 DR SMART; SM00256; FBOX.1.
 DR SMART; SM00320; WD40; 7.
 DR PROSITE; PS50181; FBOX.1.
 DR PROSITE; PS00678; WD_REPEATS_1; 5.
 DR PROSITE; PS50082; WD_REPEATS_2; 7.
 DR PROSITE; PS50294; WD_REPEATS_REGION.1.
 KW Hypothetical protein; Repeat; Ub1 conjugation pathway; WD repeat.
 SQ SEQUENCE 861 AA; 95052 MW; B5610A97A6D105FF CRC64;

Query Match 81.2%; Score 39; DB 2; Length 861;
 Best Local Similarity 75.0%; Pred. No. 55;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 HDAPVGYD 8
 DB 688 HDAPVGYD 695

RESULT 19
 05KFE2 CRYNE PRELIMINARY; PRT; 861 AA.
 AC 05KFE2;
 DT 10-MAY-2005 (TREMBLrel. 30, Created)
 DT 10-MAY-2005 (TREMBLrel. 30, Last sequence update)
 DT 10-MAY-2005 (TREMBLrel. 30, Last annotation update)
 DE Sulfur metabolite repression control protein, putative.
 GN ORFNames=CNF02050;
 OS Cryptococcus neoformans var. neoformans JEC21.
 OC Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Heterobasidiomycetes;
 OC Tremellomycetidae; Tremellales; Filobasidiella.
 CC NCBI_TaxID=214684;
 RX NCU1_TaxID=214684;
 RN [1]

RP NUCLEOTIDE SEQUENCE.
 RC STRAIN-JEC21;
 RA lotus B., Amedeo P., Roncaglia P., Vamathavan J., Uterback T.,
 RA Van Allen S., Fraser C.;
 RL Submitted (May-2004) to the EMBL/Genbank/DBJ databases.
 RN [2]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 RC STRAIN-JEC21;
 RA PubMed:15653466; DOI=10.1126/science.1103773;
 RA lotus B.J., Fung E., Roncaglia P., Rowley D., Amedeo P., Bruno D.,
 RA Vamathavan J., Miranda M., Anderson I.J., Fraser J.A., Allen J.E.,
 RA Boudet I.E., Brent M.R., Chin R., Doering T.L., Donlin M.J.,
 RA D'Souza C.A., Fox D.S., Grinberg V., Fu J., Fukushima M., Haas B.U.,
 RA Huang J.C., Janbon G., Jones S.J.M., Koo H.L., Krzywinski M.I.,
 RA Kwon-Chung K.J., Lengeler K.B., Maiti R., Marra M.A., Marra R.E.,
 RA Mathewson C.A., Mitchell T.G., Pertea M., Riggs F.R., Salzberg S.L.,
 RA Schein J.E., Shvartbeyn A., Shin H., Shumway M., Specht C.A.,
 RA Sun B.B., Tenney A., Uterback T.R., Wickes B.L., Wortman J.R.,
 RA Wye N.H., Kronstad J.W., Lodge J.K., Heltman J., Davis R.W.,
 RA Fraser C.M., Hyman R.W.;
 RT "The genome of the basidiomycetous yeast and human pathogen
 RT *Cryptococcus neoformans*."
 RL Science 307:1321-1324(2005).
 DR EMBL; AE017346; AA044020.1; -; Genomic DNA.
 DR GO; GO:0006512; P:ubiquitin cycle; IEA.
 DR InterPro; IPR001810; F-box.
 DR InterPro; IPR001680; WD40.
 DR Pfam; PF00646; F-box; 1.
 DR Pfam; PF00400; WD40; 7.
 DR PRINTS; PR00320; GPROTEINRPT.
 DR PRODOM; PD000018; WD40; 2.
 DR SMART; SM00256; FBOX; 1.
 DR SMART; SM00320; WD40; 7.
 DR PROSITE; PS0181; FBOX; 1.
 DR PROSITE; PS00678; WD_REPEATS_1; 5.
 DR PROSITE; PS0082; WD_REPEATS_2; 7.
 DR PROSITE; PS0294; WD_REPEATS_REGION; 1.
 DR Complete proteome; Repeat; Ubl conjugation pathway; WD repeat.
 KW SEQUENCE 861 AA; 95078 MW; 93393C36195EDC01 CRC64;
 SQ
 Query Match 81.2%; Score 39; DB 2; Length 861;
 Best Local Similarity 75.0%; Pred. No. 55;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1 HDAPIGYD 8
 DB 688 HDAPAGFD 695
 RESULT 20
 ID 042126 XENLA PRELIMINARY; PRT; 869 AA.
 AC 042126
 DT 01-JAN-1998 (TrEMBLrel. 05, Created)
 DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Vitellogenin receptor.
 OS *Xenopus laevis* (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
 OC Xenopodinae; Xenopus; *Xenopus*.
 OX NCBI_TaxID=8355;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Oocyte.
 RA MEDLINE=96295501; PubMed=8702402; DOI=10.1006/dbrc.1996.1040;
 RA Okabayashi K., Shoji H., Nakamura T., Hashimoto O., Aasahima M.,
 RA Sugino H.;
 RT "cDNA cloning and expression of the *Xenopus laevis* vitellogenin
 RT receptor."
 RL Biochem. Biophys. Res. Commun. 224:406-413(1996).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.

RC TISSUE=Oocyte;
 RA Okabayashi K.;
 RL Submitted (Aug-1997) to the EMBL/Genbank/DBJ databases.
 DR EMBL; AB006906; BAA22145.1; -; mRNA.
 DR PIR; JC4858; JC4858.
 DR HSP; P01130; 1A3J.
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0005509; F:calcium ion binding; IEA.
 DR GO; GO:0004872; F:receptor activity; IEA.
 DR InterPro; IPR000152; Axx hydroxyl_1_S.
 DR InterPro; IPR000742; BGF_Ca.
 DR InterPro; IPR001881; BGF_Ca.
 DR InterPro; IPR006209; BGF_Like.
 DR InterPro; IPR002172; LDL_receptor_A.
 DR InterPro; IPR000033; LDL_receptor_rep.
 DR Pfam; PF00008; EGF; 1.
 DR Pfam; PF07645; EGF_CA; 1.
 DR Pfam; PF00057; LDL_recept_8; 8.
 DR Pfam; PF00058; LDL_recept_D; 5.
 DR PRINTS; PR00261; LDLRECEPTOR.
 DR SMART; SM00179; EGF_CA; 1.
 DR SMART; SM00192; LDLR; 8.
 DR SMART; SM00135; LY; 5.
 DR PROSITE; PS00010; ASX_HYDROXYL; 2.
 DR PROSITE; PS01186; EGF_2; 3.
 DR PROSITE; PS50026; EGF_3; 2.
 DR PROSITE; PS01187; EGF_CA; 2.
 DR PROSITE; PS01209; LDLR_1; 8.
 DR PROSITE; PS50068; LDLR_2; 8.
 KW Receptor.
 KW SEQUENCE 869 AA; 96377 MW; A57A3B34072B517 CRC64;
 SQ
 Query Match 81.2%; Score 39; DB 2; Length 869;
 Best Local Similarity 75.0%; Pred. No. 56;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1 HDAPIGYD 8
 DB 371 HDPIGYE 378
 RESULT 21
 ID 06NS01 XENLA PRELIMINARY; PRT; 869 AA.
 AC 06NS01;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE VLDLR protein.
 OS *Xenopus laevis* (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
 OC Xenopodinae; Xenopus; *Xenopus*.
 OX NCBI_TaxID=8355;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Embryo;
 RA MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.B.,
 RA Brownstein M.J., Ueda T.B., Tomshycki S., Carrinci P., Prange C.,
 RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulik S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

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RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallus D.B.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.,
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Embryo;
RX MEDLINE=22341133; PubMed=12454917; DOI=10.1002/dvdy.10174;
RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA Richardson P.,
RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus
RT initiative."
RL Dev. Dyn. 225:384-391(2002).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Embryo;
RA Klein S., Strausberg R.,
RL Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC070552; AAH70552.1; -, mRNA.
DR HSPB; P01130; IAJJ.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005509; F:calcium ion binding; IEA.
DR InterPro; IPR000152; Aa hydroxyl_S.
DR InterPro; IPR000742; EGF_2.
DR InterPro; IPR001881; EGF_CA.
DR InterPro; IPR006209; EGF_like.
DR InterPro; IPR006210; IEGF.
DR InterPro; IPR002172; LDL_receptor_A.
DR InterPro; IPR000033; LDL_receptor_rep.
DR Pfam; PF00008; EGF_1.
DR Pfam; PF07645; EGF_CA; 1.
DR Pfam; PF00057; LDL_recept_a; 8.
DR Pfam; PF00058; LDL_recept_b; 5.
DR PRINTS; PR00261; LDLRECEPTOR.
DR SMART; SM00181; EGF; 6.
DR SMART; SM00179; EGF_CA; 2.
DR SMART; SM00192; LDLa; 8.
DR SMART; SM00135; LY; 5.
DR PROSITE; PS00010; ASX_HYDROXYL; 2.
DR PROSITE; PS01186; EGF_2; 3.
DR PROSITE; PS50026; EGF_3; 2.
DR PROSITE; PS01187; EGF_CA; 2.
DR PROSITE; PS01209; LDLRA_1; 8.
DR PROSITE; PS50068; LDLRA_2; 8.
SQ SEQUENCE 869 AA; 96275 MW; 232B982C275B27BD CRC64;

Query Match 81.2%; Score 39; DB 2; Length 869;
Best Local Similarity 75.0%; Pred. No. 56;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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RX MEDLINE=99428532; PubMed=10497222; DOI=10.1074/jbc.274.40.28566;
RA Quan T., Fisher G.J.;
RT "Cloning and characterization of the human protein kinase C-eta
RT promoter."
RL J. Biol. Chem. 274:28566-28574(1999).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Skin;
RA Quan T.H., Fisher G.J.;
RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Contains 1 C2 domain.
DR EMBL; AF045569; AAD12779.1; -, Genomic DNA.
DR GO; GO:0016301; F:kinase activity; IEA.
DR InterPro; IPR000008; C2.
DR Pfam; PF00168; C2; 1.
DR PRINTS; PR00360; C2DOMAIN.
DR SMART; SM00239; C2; 1.
DR PROSITE; PS50004; C2_DOMAIN_2; 1.
KW Kinase.
FT NON TER 121
SQ SEQUENCE 121 AA; 13501 MW; C913189C4A4BAF53 CRC64;

Query Match 79.2%; Score 38; DB 2; Length 121;
Best Local Similarity 62.5%; Pred. No. 11;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

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OY 1 HDAPICVD 8
DB 371 HDLPICVE 378

RESULT 22
ID 071UV9 HUMAN PRELIMINARY; PRT; 121 AA.
AC 071UV9;
DT 05-JUL-2004 (TRENDEL. 27, Created)
DT 05-JUL-2004 (TRENDEL. 27, Last sequence update)
DT 05-JUL-2004 (TRENDEL. 27, Last annotation update)
DE Protein Kinase C eta (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Skin;

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RESULT 23
ID KPC_L HUMAN STANDARD; PRT; 682 AA.
AC P24723; Q16246;
DT 01-MAR-1992 (Rel. 21, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Protein kinase C, eta type (EC 2.7.1.1-) (PKC-eta) (PKC-L).
GN Name=PRKCH; Synonyms=PKCL;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Lung;
RX MEDLINE=91094824; PubMed=1986216;
RA Bacher N., Zisman Y., Berent E., Livneh E.;
RT "Isolation and characterization of PKC-L, a new member of the protein
RT kinase C-related gene family specifically expressed in lung, skin, and
RT heart."
RL Mol. Cell. Biol. 11:126-133(1991).
RN [2]
RP ERRATUM, AND SEQUENCE REVISION.
RX MEDLINE=92186874; PubMed=1345821;
RA Bacher N., Zisman Y., Berent E., Livneh E.;
RL Mol. Cell. Biol. 12:1404-1404(1992).
RN [3]
RP NUCLEOTIDE SEQUENCE OF 437-538.
RX MEDLINE=95080426; PubMed=7988719; DOI=10.1016/0014-5793(94)01202-4;
RA Palmer R.H., Ridden U., Parker F.J.;
RT "Identification of multiple, novel, protein kinase C-related gene
RT products."
RL FEBS Lett. 356:5-8(1994).
CC -1- FUNCTION: This is calcium-independent, phospholipid-dependent,
CC serine- and threonine-specific enzyme.
CC -1- FUNCTION: PKC is activated by diacylglycerol which in turn
CC phosphorylates a range of cellular proteins. PKC also serves as
CC the receptor for photol esters, a class of tumor promoters.
CC -1- TISSUE SPECIFICITY: Most abundant in lung, less in heart and skin.
CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family. PKC

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CC      subfamily.
CC      -1- SIMILARITY: Contains 1 C2 domain.
CC      -1- SIMILARITY: Contains 2 phorbol-ester/DAG-type zinc fingers.
CC      -----
CC      This Swiss-Prot entry is copyright. It is produced through a collaboration
CC      between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC      the European Bioinformatics Institute. There are no restrictions on its
CC      use as long as its content is in no way modified and this statement is not
CC      removed.
CC      -----
CC      EMBL; M55284; AAA60100.1; -; mRNA.
CC      DR      EMBL; S74620; AAB32724.1; -; mRNA.
CC      DR      PIR; A39666; A39666.
CC      DR      HSSP; P09216; IGMI.
CC      DR      Ensemble; ENSG00000027075; Homo sapiens.
CC      DR      HGNC; HGNC:9403; PRKCH.
CC      DR      MIM; 605437; -.
CC      DR      GO; GO:0004697; F:protein kinase C activity; TAS.
CC      DR      GO; GO:0006468; P:protein amino acid phosphorylation; TAS.
CC      DR      GO; GO:0007165; P:signal transduction; TAS.
CC      DR      InterPro; IPR000008; C2.
CC      DR      InterPro; IPR002219; DAG_PE_bd.
CC      DR      InterPro; IPR000961; PKinase_C.
CC      DR      InterPro; IPR000719; Prot_kinase.
CC      DR      InterPro; IPR008271; Ser_thr_Pkin_AS.
CC      DR      InterPro; IPR002290; Ser_thr_Pkinase.
CC      DR      Pfam; PF00168; C2_1; 2.
CC      DR      Pfam; PF00069; PKinase; 1.
CC      DR      Pfam; PF00433; PKinase_C; 1.
CC      DR      PRINTS; PR00360; C2DOMAIN.
CC      DR      PRINTS; PR00008; DAGPEDOMAIN.
CC      DR      ProDom; PD000001; Prot_kinase; 1.
CC      DR      SMART; SM00109; C1; 2.
CC      DR      SMART; SM00239; S_TK_X; 1.
CC      DR      SMART; SM00133; S_TK_X; 1.
CC      DR      SMART; SM00220; S_TK_X; 1.
CC      DR      PROSITE; PS50004; C2 DOMAIN; 1.
CC      DR      PROSITE; PS50017; PROTEIN KINASE ATP; 1.
CC      DR      PROSITE; PS50011; PROTEIN KINASE DOM; 1.
CC      DR      PROSITE; PS50108; PROTEIN KINASE_ST; 1.
CC      DR      PROSITE; PS00479; ZF_DAG_PE_1; 2.
CC      DR      PROSITE; PS50081; ZF_DAG_PE_2; 2.
CC      DR      ATP-binding; Kinase; Metal-binding; Nucleotide-binding;
CC      KW      Phorbol-ester binding; Repeat; Serine/threonine-protein kinase;
CC      KW      Transferase; Zinc; zinc-finger.
CC      FT      DOMAIN 12 112 C2..
CC      FT      ZN_FING 354 613 Protein kinase.
CC      FT      ZN_FING 170 221 Phorbol-ester/DAG-type 1.
CC      FT      ZN_FING 244 294 Phorbol-ester/DAG-type 2.
CC      FT      NP_BIND 360 368 ATP (By similarity).
CC      FT      ACT_SITE 478 478 Proton acceptor (By similarity).
CC      FT      BINDING 383 383 ATP (By similarity).
CC      FT      CONFLICT 471 471 D -> B (in Ref. 3).
CC      SQ      SEQUENCE 682 AA; 77563 MW; 13D4EAB013B5AB8 CRC64;

Query Match      79.2%; Score 38; DB 1; Length 682;
Beet Local Similarity 62.5%; Pred. No. 70;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy      1 HDAPITGYD 8
Db      88 HETPIGYD 95

RESULT 24
KCTL_MOUSE      STANDARD; PRT; 683 AA.
AC      P23358;
DT      01-NOV-1991 (rel. 20, Last sequence update)
DT      13-SEP-2005 (rel. 48, Last annotation update)
DR      Protein kinase C, eta type (EC 2.7.1.1-) (nPKC-eta) (PKC-L).

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GN      Name=Prkch; Synonyms=Pchh;
OS      Mus musculus (Mouse).
OC      Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC      Muridae; Muridae; Murinae; Mus.
OX      NCBI_TaxId=10090;
RN      [1]
RP      NUCLEOTIDE SEQUENCE [mRNA].
RC      TISSUE=Epidermis;
RX      MEDLINE=91093089; PubMed=2266135;
RA      Osada S.I., Mizuno K., Saido T.C., Akita Y., Suzuki K., Kuroki T.,
RA      Ohno S.;
RT      "A phorbol ester receptor/protein kinase, nPKC eta, a new member of
RT      the protein kinase C family predominantly expressed in lung and
RT      skin.";
RL      J. Biol. Chem. 265:22434-22440(1990).
CC      -1- FUNCTION: This is calcium-independent, phospholipid-dependent,
CC      serine- and threonine-specific enzyme.
CC      -1- FUNCTION: PKC is activated by diacylglycerol which in turn
CC      phosphorylates a range of cellular proteins. PKC also serves as
CC      the receptor for phorbol esters, a class of tumor promoters.
CC      -1- TISSUE SPECIFICITY: Predominantly expressed in lung and skin.
CC      -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family. PKC
CC      subfamily.
CC      -1- SIMILARITY: Contains 1 C2 domain.
CC      -1- SIMILARITY: Contains 2 phorbol-ester/DAG-type zinc fingers.
CC      -----
CC      This Swiss-Prot entry is copyright. It is produced through a collaboration
CC      between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC      the European Bioinformatics Institute. There are no restrictions on its
CC      use as long as its content is in no way modified and this statement is not
CC      removed.
CC      -----
CC      EMBL; D90242; BAAL4288.1; -; mRNA.
CC      DR      PIR; A23690; A23690.
CC      DR      HSSP; P28867; IPTO.
CC      DR      Ensemble; ENSMUSG00000021108; Mus musculus.
CC      DR      MGI; MGI:97600; Prkch.
CC      DR      InterPro; IPR000008; C2.
CC      DR      InterPro; IPR002219; DAG_PE_bd.
CC      DR      InterPro; IPR000961; PKinase_C.
CC      DR      InterPro; IPR000719; Prot_kinase.
CC      DR      InterPro; IPR008271; Ser_thr_Pkin_AS.
CC      DR      InterPro; IPR002290; Ser_thr_Pkinase.
CC      DR      Pfam; PF00130; C1_1; 2.
CC      DR      Pfam; PF00168; C2; 1.
CC      DR      Pfam; PF00069; PKinase; 1.
CC      DR      Pfam; PF00433; PKinase_C; 1.
CC      DR      PRINTS; PR00360; C2DOMAIN.
CC      DR      PRINTS; PR00008; DAGPEDOMAIN.
CC      DR      ProDom; PD000001; Prot_kinase; 1.
CC      DR      SMART; SM00109; C1; 2.
CC      DR      SMART; SM00239; C2; 1.
CC      DR      SMART; SM00133; S_TK_X; 1.
CC      DR      SMART; SM00220; S_TK_X; 1.
CC      DR      PROSITE; PS50004; C2 DOMAIN; 1.
CC      DR      PROSITE; PS50017; PROTEIN KINASE ATP; 1.
CC      DR      PROSITE; PS50011; PROTEIN KINASE DOM; 1.
CC      DR      PROSITE; PS50108; PROTEIN KINASE_ST; 1.
CC      DR      PROSITE; PS00479; ZF_DAG_PE_1; 2.
CC      DR      PROSITE; PS50081; ZF_DAG_PE_2; 2.
CC      DR      ATP-binding; Kinase; Metal-binding; Nucleotide-binding;
CC      KW      Phorbol-ester binding; Repeat; Serine/threonine-protein kinase;
CC      KW      Transferase; Zinc; zinc-finger.
CC      FT      DOMAIN 12 102 C2.
CC      FT      ZN_FING 355 614 Protein kinase.
CC      FT      ZN_FING 171 222 Phorbol-ester/DAG-type 1.
CC      FT      ZN_FING 245 295 Phorbol-ester/DAG-type 2.
CC      FT      NP_BIND 361 369 ATP (By similarity).
CC      FT      ACT_SITE 479 479 Proton acceptor (By similarity).
CC      FT      BINDING 384 384 ATP (By similarity).
CC      SQ      SEQUENCE 683 AA; 77974 MW; CTDB338A9F95576 CRC64;

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Query Match          79.2%; Score 38; DB 1; Length 683;
Best Local Similarity 62.5%; Pred. No. 70;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY      1 HDAPICVD 8
Db      88 HETPLGYD 95

RESULT 25
KPCCL RAT          STANDARD; PRT; 683 AA.
ID      KPCCL RAT
AC      O64617;
DT      01-NOV-1997 (Rel. 35, Created)
DT      01-NOV-1997 (Rel. 35, Last sequence update)
DT      13-SEP-2005 (Rel. 48, Last annotation update)
DE      Protein Kinase C, eta type (EC 2.7.1.1-) (PKC-eta) (PKC-L).
GN      Name=Prkch; Synonym=PKch;
OS      Rattus norvegicus (Rat).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC      Muridae; Muridae; Murinae; Rattus.
OX      NCBI_TaxID=10116;
RN      [1]
RP      NUCLEOTIDE SEQUENCE [MRNA].
RC      STRAIN=Sprague-Dawley; TISSUE=Lung;
RX      MEDLINE=93050193; PubMed=1426252; DOI=10.1016/0014-5793(92)80934-9;
RA      Dekker L.V., Parker P.J., McIntyre P.;
RT      "Biochemical properties of rat protein kinase C-eta expressed in COS
      cells.";
RL      FEBS Lett. 312:195-199(1992).
RN      [2]
RP      NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RC      TISSUE=Lung;
RG      NIH - Mammalian Gene Collection (MGC) project;
RL      Submitted (SEP-2004) to the EMBL/GenBank/DBJ databases.
CC      -1- FUNCTION: This is calcium-independent, phospholipid-dependent,
      CC      serine- and threonine-specific enzyme.
      CC      -1- FUNCTION: PKC is activated by diacylglycerol which in turn
      CC      phosphorylates a range of cellular proteins. PKC also serves as
      CC      the receptor for phorbol esters, a class of tumor promoters.
      CC      -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family. PKC
      CC      subfamily.
      CC      -1- SIMILARITY: Contains 1 C2 domain.
      CC      -1- SIMILARITY: Contains 2 phorbol-ester/DAG-type zinc fingers.
      CC      -----
      CC      This Swiss-Prot entry is copyright. It is produced through a collaboration
      CC      between the Swiss Institute of Bioinformatics and the EMBL outstation -
      CC      the European Bioinformatics Institute. There are no restrictions on its
      CC      use as long as its content is in no way modified and this statement is not
      CC      removed.
      CC      -----
      CC      -----
      CC      EMBL; X68400; CAA48466.1; -; mRNA.
      DR      EMBL; BC081782; AAH81782.1; -; mRNA.
      DR      PIR; I60246; S29478.
      DR      HSSP; P28867; IPTO.
      DR      Ensembl; ENSRNOG0000004873; Rattus norvegicus.
      DR      RGD; 621888; Prkch.
      DR      GO; GO:0004672; F:protein kinase activity; IDA.
      DR      GO; GO:0006468; P:protein amino acid phosphorylation; IDA.
      DR      InterPro; IPR000008; C2.
      DR      InterPro; IPR002219; DAG_PE_bd.
      DR      InterPro; IPR000961; PKinase_C.
      DR      InterPro; IPR000719; Prot_Kinase.
      DR      InterPro; IPR008271; Ser_thr_pkin_AS.
      DR      InterPro; IPR002290; Ser_thr_pkinase.
      DR      Pfam; PF00130; C1.1. 2.
      DR      Pfam; PF00168; C2.1.
      DR      Pfam; PF00063; Kinase; 1.
      DR      Pfam; PF00433; Kinase_C; 1.
      DR      PRINTS; PR00360; C2DOMAIN.
      DR      PRINTS; PR00008; DAGPEDOMAIN.
      DR      ProDom; PD000001; Prot_kinase; 1.

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DR      SMART; SM00109; C1; 2.
DR      SMART; SM00239; C2; 1.
DR      SMART; SM00133; S_TK_X; 1.
DR      SMART; SM00220; S_TKC; 1.
DR      PROSITE; PS50004; C2_DOMAIN; 1.
DR      PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR      PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR      PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
DR      PROSITE; PS00479; ZF_DAG_PE_1; 2.
DR      PROSITE; PS50081; ZF_DAG_PE_2; 2.
KW      ATP-binding; Kinase; Metal-Binding; Nucleotide-binding;
KW      Phorbol-ester binding; Repeat; Serine/threonine-protein kinase;
KW      Transferase; Zinc; Zinc-finger.
FT      DOMAIN          12 102
FT      ZN_FING         355 614
FT      ZN_FING         171 222
FT      ZN_FING         245 295
FT      NP_BIND         361 369
FT      ACT_SITE        479 479
FT      BINDING         384 384
SQ      SEQUENCE        683 AA; 77947 MW; 2F5B7078D1206510 CRC64;

Query Match          79.2%; Score 38; DB 1; Length 683;
Best Local Similarity 62.5%; Pred. No. 70;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY      1 HDAPICVD 8
Db      88 HETPLGYD 95

RESULT 26
O8NE03 HUMAN
ID      O8NE03;
AC      O8NE03;
DT      01-OCT-2002 (TREMBLrel. 22, Created)
DT      01-OCT-2002 (TREMBLrel. 22, Last sequence update)
DT      01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE      Protein kinase C, eta.
GN      Name=PRKCH;
OS      Homo sapiens (Human).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC      Homo.
OX      NCBI_TaxID=9606;
RN      [1]
RP      NUCLEOTIDE SEQUENCE.
RC      TISSUE=Testis;
RX      MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA      Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA      Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA      Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA      Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Halel P.,
RA      Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA      Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA      Brownstein M.J., Ueidi T.B., Tohyuki S., Carninci P., Prange C.,
RA      Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA      Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA      Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulik S.W.,
RA      Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA      Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA      Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA      Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA      Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA      Buterfield Y.S.N., Krzywinski M.I., Skalek U., Smalhus D.E.,
RA      Butcher A., Schein J.E., Jones S.J.M., Marra M.A.;
RT      "Generation and initial analysis of more than 15,000 full-length human
      RT      and mouse cDNA sequences.";
RL      Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN      [2]
RP      NUCLEOTIDE SEQUENCE.
RC      TISSUE=Testis;
RG      NIH MGC Project;

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OC Pteromalidae; Pteromalinae; Nasonia.
OX NCBI_TaxID=7425;
RN RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=93196484; PubMed=83873793;
RA Burke W.D., Eickbush D.G., Xiong Y., Jakubczak J.L., Eickbush T.H.;
RT "Sequence relationship of retrotransposable elements R1 and R2 within
    and between divergent insect species."
RL Mol. Biol. Evol. 10:163-185(1993).
RN [2]
RP SEQUENCE REVISION.
RA Burke W.D., Eickbush D.G., Xiong Y., Jakubczak J.L., Eickbush T.H.;
RT submitted (AUG-1997) to the EMBL/Genbank/DBJ databases.
CC -1- CATALYTIC ACTIVITY: Deoxynucleoside triphosphate + DNA(n) =
    diphosphate + DNA(n+1).
CC -1- SIMILARITY: Contains 1 C2H2-type zinc finger.
CC -1- SIMILARITY: Contains 1 reverse transcriptase domain.
CC CC This Swiss-Prot entry is copyright. It is produced through a collaboration
    between the Swiss Institute of Bioinformatics and the EMBL outstation -
    the European Bioinformatics Institute. There are no restrictions on its
    use as long as its content is in no way modified and this statement is not
    removed.
CC -----
DR EMBL, L00950; AAC34927.1; -; Genomic_DNA.
DR PIR, T10259; T10259.
DR InterPro; IPR000477; RVTse.
DR InterPro; IPR01087; ZnF_C2H2.
DR Pfam; PF00078; RVT_1; 1.
DR SMART; SM00355; ZnF_C2H2; 1.
DR PROSITE; PS50878; RT_POL; 1.
DR PROSITE; PS50028; ZINC_FINGER_C2H2_1; 1.
DR PROSITE; PS50157; ZINC_FINGER_C2H2_2; 1.
DR KX Endonuclease; Hydroxase; Metal-binding; Nuclease;
    KM Nucleotidyltransferase; RNA-directed DNA polymerase; Transferase;
    Transposable element; Zinc; zinc-finger.
FT DOMAIN 358 635 Reverse transcriptase.
FT ZN_FING 46 69 C2H2-type.
FT REGION 755 1025 Nucleic acid-binding endonuclease.
FT NON_TER 1 1
SQ SEQUENCE 1025 AA; 115885 MW; 387BDE63BCF5C518 CRC64;

Query Match 79.2% Score 38; DB 1; Length 1025;
Best Local Similarity 85.7% Pred. No. 1.1e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 HDARIGY 7
DB 709 HDRPIGY 715

RESULT 29
OAKB20 PSEFS
ID OAKB20_PSEFS PRELIMINARY; PRT; 379 AA.
CC OAKB20;
DT 13-SEP-2005 (TREMBlrel. 31, Created)
DT 13-SEP-2005 (TREMBlrel. 31, Last sequence update)
DT 13-SEP-2005 (TREMBlrel. 31, Last annotation update)
DE Acetyltransferase, GNAT family family.
GN ORFNames=PFL_3459;
OS Pseudomonas fluorescens (strain Pf-5).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
    Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=220664;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Pf-5;
RC PubMed=15980861; DOI=10.1038/nbt1110;
RA Paulsen I.T., Press C., Ravel J., Kobayashi D., Myers G.S.,
    Mayroodi D., DeBoy R.T., Sehadri R., Ren Q., Madupu R., Dodson R.J.,
    Durkin S., Brinkac L.M., Daugherty S.C., Sullivan S.A., Rosovitz M.,
    Gwinn M.L., Zhou L., Nelson W.C., Weidman J., Watkins K., Tran K.,
    Khouri H.M., Plesion E., Plesion L., Thomasow L., Loper J.;

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RT "Complete genome sequence of the plant commensal Pseudomonas
RT fluorescens Pf-5."
RL Nat. Biotechnol. 23:873-878(2005).
DR EMBL; CP000076; AAY92727.1; -; Genomic_DNA.
KW Transferrase.
SQ SEQUENCE 379 AA; 43072 MW; F8BE37F559CAEF8A CRC64;

Query Match 77.1%; Score 37; DB 2; Length 379;
Best Local Similarity 71.4%; Pred. No. 60;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 HDAP1GY 7
|||:|
Db 148 HDAPVGF 154

RESULT 30
O44320_HIPCN PRELIMINARY; PRT; 493 AA.
AC O44320;
DT 01-JUN-1998 (TREMBlrel. 06, Created)
DT 01-JUN-1998 (TREMBlrel. 06, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Reverse transcriptase (Fragment).
GN Name=R2 ORF;
OS Hippodamia convergens (Convergent lady beetle).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Coleoptera; Polyphaga; Cuculiformia;
OC Coccinellidae; Coccinellinae; Coccinellini; Hippodamia.
OX NCBI_TaxID=64696;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Burke W.D., Malik H.S., Eickbush T.H.;
RL Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF015816; AAB94040.1; -; Genomic_DNA.
DR GO; GO:0003723; P:RNA binding; IEA.
DR GO; GO:0003964; P:RNA-directed DNA polymerase activity; IEA.
DR GO; GO:0016740; E:transferase activity; IEA.
DR GO; GO:0006278; P:RNA-dependent DNA replication; IEA.
KW RNA-directed DNA polymerase.
FT NON TER 1
SQ SEQUENCE 493 AA; 55882 MW; 9F776B92C636B9C9 CRC64;

Query Match 77.1%; Score 37; DB 2; Length 493;
Best Local Similarity 71.4%; Pred. No. 80;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 HDAP1GY 7
|||:|
Db 159 HDAPVGF 165

RESULT 31
O4P6X8_USTMA PRELIMINARY; PRT; 685 AA.
ID O4P6X8;
AC O4P6X8;
DT 13-SEP-2005 (TREMBlrel. 31, Created)
DT 13-SEP-2005 (TREMBlrel. 31, Last sequence update)
DT 13-SEP-2005 (TREMBlrel. 31, Last annotation update)
DE Hypothetical protein.
GN ORFNames=OM00635.1;
OS Ustilago maydis 521.
OC Eukaryota; Fungi; Basidiomycota; Ustilaginomycetes;
OC Ustilaginomycetidae; Ustilaginales; Ustilaginaceae; Ustilago.
OX NCBI_TaxID=237631;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=521;
RA Biren B., Nisbaum C., Abebe A., Abouelleil A., Adekoya B.,
RA Alt-zaira M., Allen T., An P., Anderson M., Anderson S.,
RA Archchi H., Ambuster J., Bachtsang P., Baldwin J., Barry A.,
RA Bayul T., Biltsteyn B., Bloom T., Blye J., Boguslavsky L.,
RA Botwery M., Bouhagalter B., Brunache A., Butler J., Calixte N.,

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RA Calvo S., Camarata J., Campo K., Chang J., Cheeshaens Y., Citroen M.,
RA Collamore A., Conside T., Cook A., Cooke P., Corum B., Cuomo C.,
RA David L., Dawe T., Degray S., Dodge S., Dooley K., Dorje P.,
RA Dorjee K., Dorris L., Duffey N., Dupes A., Elkins T., Engels R.,
RA Erickson J., Farina A., Faro S., Ferreira P., Fischer H.,
RA Fitzgerald M., Foley K., Gage D., Galagan J., Geatin G., Gierre S.,
RA Gitzke A., Goyette A., Graham J., Grandbois E., Gyalsen K., Hafez N.,
RA Hagopian D., Hagos B., Hall J., Hatcher B., Heller A., Higgins H.,
RA Hagan T., Horn A., Houde N., Hughes L., Hulme W., Huby B., Iliev I.,
RA Jaffe D., Jones C., Kamel M., Kamat A., Kamysellis M., Karlsson E.,
RA Kells C., Kieu A., Kiser P., Kodira C., Kulbokas E., Labutit K.,
RA Lama D., Landers T., Leger J., Levine S., Lewis D., Lewis T.,
RA Lindblad-coh K., Liu X., Lokytang T., Lokytang Y., Lucien O.,
RA Lui A., Ma L.-J., Mabbitt R., Macdonald J., Maclean C., Major J.,
RA Manning J., Marabella R., Maru K., Matthews C., Mauceli E.,
RA McCarthy M., McDonough S., Mcgee T., Meldrum J., Menus L.,
RA Mestrov J., Mihalev A., Minova T., Mikkelsen T., Mlenga V., Moru K.,
RA Moses J., Mulrain L., Munson G., Naylor J., Neves C., Nguyen C.,
RA Nguyen N., Nguyen T., Nicol R., Nielsen C., Nizari M., Norbu C.,
RA Norbu N., O'donnell P., Okawa O., O'leary S., Omotosho B.,
RA O'Neill K., Osman S., Parker S., Perrin D., Phunkhang P., Piquani B.,
RA Purcell S., Rachupka T., Ramasamy U., Rameau R., Ray V., Raymond C.,
RA Retta R., Richardson S., Rise C., Rodriguez J., Rogers J., Rogov P.,
RA Rutman M., Schubach R., Seaman C., Settipalli S., Sharpe T.,
RA Sheridan J., Sherpa N., Shi J., Shtinov S., Smith C., Sougnaz C.,
RA Spencer B., Stalker J., Stange-thomann N., Stavropoulos S.,
RA Steison K., Stone S., Stone S., Stubbs M., Talama J., Tehunga P.,
RA Tenzing P., Tesfaye S., Theodore J., Thouloung Y., Topham K.,
RA Toney S., Tsamla T., Tecmo N., Vallee D., Vassiliou H.,
RA Venkateraman V., Vinson J., Vo A., Wade C., Wang S., Wangchuk T.,
RA Wangdi T., Whitaker C., Wilkinson J., Wu Y., Wyman D., Yadev S.,
RA Yang S., Yang X., Yeager S., Yee B., Young G., Zainoun J., Zembeck L.,
RA Zimmer A., Zody M., Lander E.,
RA "The genome sequence of *Ustilago maydis*."
RL Submitted (FEB-2004) to the EMBL/Genbank/DDBJ databases.
CC -1- CAUTION: The sequence shown here is derived from an
CC EMBL/Genbank/DDBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
CC EMBL/AACP01000015; EAK01064.1; - Genomic DNA.
DR Hypothetical protein.
KM
SQ SEQUENCE 685 AA; 74135 MW; BD622893463B10E2 CRC64;

Query Match 77.1%; Score 37; DB 2; Length 685;
Best Local Similarity 71.4%; Pred. No. 1.1e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 HDAPVGY 7
|:|:|:|
DB 269 HDAPVGY 275

RESULT 32
O91WX8.RAT PRELIMINARY; PRT; 695 AA.
AC O91WX8;
DT 01-DEC-2001 (TRENBLREL. 19, Created)
DT 01-DEC-2001 (TRENBLREL. 19, Last sequence update)
DT 01-JUN-2002 (TRENBLREL. 21, Last annotation update)
DE Voltage-gated calcium channel pore forming subunit Cav1.3alpha1
DE (Fragment).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Rattus.
OC NCBI_TaxID=10116;
OX RN
RN [1]
RP NUCLEOTIDE SEQUENCE.
RP STRAIN-Sprengue-Dawley; TISSUE=superior cervical ganglia;
RX MEDLINE=21380268; PubMed=11487617;
RX Xu W., Lipscombe D.;
RT "Neuronal Ca(V)1.3alpha(1) L-type channels activate at relatively
RT hyperpolarized membrane potentials and are incompletely inhibited by
RT dihydropyridines.";

RL J. Neurosci. 21:5944-5951(2001).
DR EMBL; AF370010; AA072960.1; -; mRNA.
DR EMBL; ENSRNOG0000013147; Rattus norvegicus.
FT NON TRAN 1
SQ SEQUENCE 695 AA; 79033 MW; B9A5A1CE11FB7D32 CRC64;

Query Match 77.1%; Score 37; DB 2; Length 695;
Best Local Similarity 85.7%; Pred. No. 1.2e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 2 DAPIGYD 8
|:|:|:|
DB 429 DAPIGYD 435

RESULT 33
CACID.RAT STANDARD; PRT; 2203 AA.
AC P27732; 009022; 009023; 009024; 001542; Q62691; Q62815; Q63491;
AC Q63492;
DT 01-OCT-1996 (Rel. 34, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Voltage-dependent L-type calcium channel alpha-1D subunit (Voltage-
DE gated calcium channel alpha subunit Cav1.3) (Calcium channel, L type,
DE alpha-1 polypeptide, isoform 2) (Rat brain class D) (RBD).
GN Name=Cacal1d; Synonyms=Cacch3, Cacn4, Cacn1a2, Cc11a2;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP NUCLEOTIDE SEQUENCE (ISOFORMS 1 AND 2).
RC TISSUE=Insulinoma;
RX MEDLINE=95280950; PubMed=7760845; DOI=10.1210/me.9.1.121;
RX Ihara Y., Yamada Y., Fujii Y., Gonoi T., Yano H., Yasuda K.,
RX Inagaki N., Saito Y., Saito S.;
RT "Molecular diversity and functional characterization of voltage-
RT dependent calcium channels (CACN4) expressed in pancreatic beta-
RT cells."
RT Mol. Endocrinol. 9:121-130(1995).
RL
RN [2]
RP NUCLEOTIDE SEQUENCE (ISOFORMS 3, 6, 7, 8 AND 13).
RC TISSUE=Brain;
RX MEDLINE=91299338; PubMed=1648940; DOI=10.1016/0896-6273(91)90072-8;
RX Hui A., Billnor P.T., Krizanova O., Wang J.-J., Diebold R.J.,
RX Schwartz A.;
RT "Molecular cloning of multiple subtypes of a novel rat brain isoform
RT of the alpha-1 subunit of the voltage-dependent calcium channel."
RT Neuron 7:35-44(1991).
RN [3]
RP NUCLEOTIDE SEQUENCE OF 1-125.
RX MEDLINE=96040125; PubMed=7553731;
RX Kamp T.J., Milas M., Fields K.L., Aesch S., Chin H., Marban E.,
RX Nirenberg M.;
RT "Transcriptional regulation of the neuronal L-type calcium channel
RT alpha 1D subunit gene."
RT Cell. Mol. Neurobiol. 15:307-326(1995).
RN [4]
RP NUCLEOTIDE SEQUENCE OF 1100-1410 (ISOFORMS 4 AND 11).
RC TISSUE=Kidney;
RX MEDLINE=93066265; PubMed=1279681;
RX Yu A.S.L., Hebert S.C., Brenner B.M., Lytton J.;
RT "Molecular characterization and nephron distribution of a family of
RT transcripts encoding the pore-forming subunit of Ca2+ channels in the
RT kidney."
RT Proc. Natl. Acad. Sci. U.S.A. 89:10494-10498(1992).
RN [5]
RP NUCLEOTIDE SEQUENCE OF 1218-1498 (ISOFORM 12).
RC TISSUE=Osteocarcinoma;
RX MEDLINE=96074617; PubMed=7479909;
RX Barry E.L.R., Geesek F.A., Froehner S.C., Friedman P.A.;

"Multiple calcium channel transcripts in rat osteosarcoma cells: selective activation of alpha 1D isoform by parathyroid hormone.;"
Proc. Natl. Acad. Sci. U.S.A. 92:10914-10918(1995).
[6]
Nucleotide Sequence of 1200-1493 (ISOFORMS 3, 4, 5, 9 AND 10).
RC TISSUE=Hepatoma;
MEDLINE=97376179; PubMed=9232351; DOI=10.1016/S0143-160(97)90088-9;
RA Breerem H.M., Harland M.L., Froscio M., Petronijevic T.,
RA Barrett G.J.;
RT "Novel variants of voltage-operated calcium channel alpha-1 subunit transcripts in a rat liver-derived cell line: deletion in the IVS4 voltage sensing region.;"
Cell Calcium 22:39-52(1997).
[7]
NP NUCLEOTIDE SEQUENCE OF 1307-1479 (ISOFORM 3).
RX MEDLINE=90239020; PubMed=1692134;
RA Snutch T.P., Leonard J.P., Gilbert M.M., Lester H.A., Davidson N.,
RT "Rat brain expresses a heterogeneous family of calcium channels.;"
Proc. Natl. Acad. Sci. U.S.A. 87:3391-3395(1990).
CC -1- FUNCTION: Voltage-sensitive calcium channels (VSCC) mediate the entry of calcium ions into excitable cells and are also involved in a variety of calcium-dependent processes, including muscle contraction, hormone or neurotransmitter release, gene expression, cell motility, cell division and cell death. The isoform alpha-1D gives rise to L-type calcium currents. Long-lasting (L-type) calcium channels belong to the "high-voltage activated" (HVA) group. They are blocked by dihydropyridines (DHP), and by omega-agatoxin-IIIa phenylalylamines, benzothiazepines, and by omega-conotoxin-IIIa (omega-Aga-IIIa). They are however insensitive to omega-conotoxin-GVIA (omega-CTX-GVIA) and omega-agatoxin-IVA (omega-Aga-IVA).
CC -1- SUBUNIT: Voltage-dependent calcium channels are multisubunit complexes, consisting of alpha-1, alpha-2, beta and delta subunits in a 1:1:1:1 ratio. The channel activity is directed by the pore-forming and voltage-sensitive alpha-1 subunit. In many cases, this subunit is sufficient to generate voltage-sensitive calcium channel activity. The auxiliary subunits beta and alpha-2/delta linked by a disulfide bridge regulate the channel activity.
CC Interacts with RIMBP2 (By similarity).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=13;
CC Comment=The region sequenced in isoforms ROB3 and RKC5 is identical to CACNA4;
CC Name=1; Synonym=CACNA4;
CC IsoId=P27732-1; Sequence=Displayed;
CC Name=2; Synonym=CACNA4B;
CC IsoId=P27732-2; Sequence=VSP_000923; VSP_000924;
CC Name=3; Synonym=CACNA3A, RB48, RBD-55;
CC IsoId=P27732-3; Sequence=VSP_000921;
CC Name=4; Synonym=Delta-IV-S3, RKC6;
CC IsoId=P27732-4; Sequence=VSP_000919;
CC Name=5; Synonym=Delta-IV-S4;
CC IsoId=P27732-5; Sequence=VSP_000922;
CC Name=6; Synonym=RB9;
CC IsoId=P27732-6; Sequence=VSP_000920, VSP_000921;
CC Name=7; Synonym=RB11;
CC IsoId=P27732-7; Sequence=VSP_000917;
CC Name=8; Synonym=RB34;
CC IsoId=P27732-8; Sequence=VSP_000916;
CC Name=9; Synonym=RB1;
CC IsoId=P27732-9; Sequence=VSP_000918;
CC Name=10; Synonym=RB2;
CC IsoId=P27732-10; Sequence=VSP_000919, VSP_000922;
CC Name=11; Synonym=RKC5;
CC IsoId=P27732-13; Sequence=Not described;
CC Name=12; Synonym=ROB3;
CC IsoId=P27732-14; Sequence=Not described;
CC Name=13; Synonym=Truncated;
CC IsoId=P27732-12; Sequence=VSP_000925, VSP_000926;
CC -1- TISSUE SPECIFICITY: Expressed in brain, pancreatic islets and B-lymphocytes.
CC -1- DOMAIN: Each of the four internal repeats contains five hydrophobic transmembrane segments (S1, S2, S3, S5, S6) and one

CC positively charged transmembrane segment (S4). S4 segments
CC serbially represent the voltage-sensor and are characterized by a
CC series of positively charged amino acids at every third position.
CC -1- SIMILARITY: Belongs to the calcium channel alpha-1 subunit family.
CC -----
CC This Swiss-Prot entry is copyrighted. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC EMBL; D38101; BAA07282.1; -; mRNA.
CC EMBL; D38102; BAA07283.1; -; mRNA.
CC EMBL; M57682; AAA42015.1; -; mRNA.
CC EMBL; U14005; AAB60515.1; -; Genomic_DNA.
CC EMBL; M99221; AAA40895.1; -; mRNA.
CC EMBL; U13772; AAB89156.1; -; mRNA.
CC EMBL; U49126; AAB61634.1; -; mRNA.
CC EMBL; U49127; AAB61635.1; -; mRNA.
CC EMBL; U49128; AAB61636.1; -; mRNA.
CC Ensemble: ENSRNOG00000013147; Rattus norvegicus.
CC RGD; 70973; Cactaid.
CC DR GO; GO:0005891; C:Voltage-gated calcium channel complex; TAS.
CC DR GO; GO:0005245; F:Voltage-gated calcium channel activity; IDA.
CC DR GO; GO:0019722; P:calcium-mediated signalling; IDA.
CC DR InterPro; IPR001682; Ca/Na pore.
CC DR InterPro; IPR002077; Ca channel alpha.
CC DR InterPro; IPR002111; Cat_channel_TPL.
CC DR InterPro; IPR001992; EF-Hand type.
CC DR InterPro; IPR005821; Ion trans.
CC DR InterPro; IPR003091; K channel.
CC DR InterPro; IPR005446; LVDCCALpha1.
CC DR InterPro; IPR005820; M+channel_nlg.
CC DR Pfam; PF00520; Ion_trans; 4.
CC DR PRINTS; PR00167; KCHANNEL.
CC DR PRINTS; PR00169; KCHANNEL.
CC DR PRINTS; PR01630; LVDCCALPHA1.
CC DR PRINTS; PR01636; LVDCCALPHA1D.
CC KW Alternative splicing; Calcium; Calcium channel; Calcium transport;
CC KW Glycoprotein; Ion transport; Ionic channel; Multigene family;
CC KW Phosphorylation; Repeat; Transmembrane; Transport;
CC KW Voltage-gated channel.
CC FT TOPO_DOM 1 126
CC FT TRANSMEM 127 145 Cytoplasmic (Potential).
CC FT TOPO_DOM 146 163 S1 of repeat I (Potential).
CC FT TRANSMEM 164 183 Extracellular (Potential).
CC FT TOPO_DOM 184 195 S2 of repeat I (Potential).
CC FT TRANSMEM 196 214 Cytoplasmic (Potential).
CC FT TOPO_DOM 215 235 S3 of repeat I (Potential).
CC FT TRANSMEM 236 254 Extracellular (Potential).
CC FT TOPO_DOM 255 273 S4 of repeat I (Potential).
CC FT TRANSMEM 274 293 Cytoplasmic (Potential).
CC FT TOPO_DOM 294 381 S5 of repeat I (Potential).
CC FT TRANSMEM 382 406 Extracellular (Potential).
CC FT TOPO_DOM 407 582 S6 of repeat I (Potential).
CC FT TRANSMEM 583 602 Cytoplasmic (Potential).
CC FT TOPO_DOM 603 617 S1 of repeat II (Potential).
CC FT TRANSMEM 618 636 Extracellular (Potential).
CC FT TOPO_DOM 637 644 S2 of repeat II (Potential).
CC FT TRANSMEM 645 663 Cytoplasmic (Potential).
CC FT TOPO_DOM 664 673 S3 of repeat II (Potential).
CC FT TRANSMEM 674 692 Extracellular (Potential).
CC FT TOPO_DOM 693 711 S4 of repeat II (Potential).
CC FT TRANSMEM 712 732 Cytoplasmic (Potential).
CC FT TOPO_DOM 733 752 S5 of repeat II (Potential).
CC FT TRANSMEM 753 786 Extracellular (Potential).
CC FT TOPO_DOM 787 811 S6 of repeat II (Potential).
CC FT TRANSMEM 812 945 Cytoplasmic (Potential).
CC FT TOPO_DOM 946 964 S1 of repeat III (Potential).
CC FT TRANSMEM 965 980 Extracellular (Potential).
CC FT TOPO_DOM 981 1000 S2 of repeat III (Potential).
CC Query Match 77.1%; Score 37; DB 1; Length 2203;

Best Local Similarity 85.7%; Pred. No. 4e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 DAPIGYD 8
Db 1937 DSPGYD 1943

RESULT 34
Q6D7L9 ERWCT PRELIMINARY; PRT; 213 AA.
ID Q6D7L9 ERWCT PRELIMINARY; PRT; 213 AA.
AC Q6D7L9 ERWCT PRELIMINARY; PRT; 213 AA.
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Nucleotide-nucleotide adenylyltransferase (Conserved hypothetical protein) (EC 2.7.7.18).
GN Name: nadt, OrderedLocustNames:BCA1306;
OS *Erwinia carotovora* (subsp. atroseptica) (Pectobacterium atrosepticum).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Pectobacterium.
OX NCBI_TaxID=29471;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=SCRI 1043 / ATCC BAA-672;
RX PubMed=15263089; DOI=10.1073/pnas.040242101;
RA Bell K.S., Sebaldia M., Pritchard L., Holden M.T.G., Hyman L.J.,
RA Holva M.C., Thomson N.R., Bentley S.D., Churcher L.J.C., Mungall K.,
RA Atlin R., Baron N., Brooks K., Chillingworth T., Clark K., Doggett J.,
RA Fraser A., Hance Z., Hauser H., Jagsels K., Moule S., Norbertczak H.,
RA Ormond D., Price C., Quail M.A., Sanders M., Walker D., Whitehead S.,
RA Salmond G.P.C., Birch P.R.V., Parkhill J., Toth I.K.;
RT "Genome sequence of the enterobacterial phytopathogen *Erwinia carotovora* subsp. atroseptica and characterization of virulence factors.";
RT Proc. Natl. Acad. Sci. U.S.A. 101:11105-11110(2004).
RL EMBL, BX950851; CNG74216.1; -; Genomic DNA.
DR GO; GO:0004515; F:nucleotide-nucleotide adenylyltransferase a. . .; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0009058; P:biogenesis; IEA.
DR GO; GO:0009435; P:NAD biosynthesis; IEA.
DR InterPro; IPR004820; Cytidylyltransf.
DR InterPro; IPR004821; Cytidylyltransf.
DR InterPro; IPR005248; NAMN_adnstrase.
DR Pfam; PF01467; CTP_transf. 2; 1.
DR TIGRFAMs; TIGR00125; cyt_tran_rel. 1.
DR TIGRFAMs; TIGR00482; NAMN_adnstrase; 1.
KW Complete proteome; Hypothetical protein; Nucleotidyltransferase;
KW Transferrase.
SQ SEQUENCE 213 AA; 24208 MW; C7C3DBFF68941E9C CRC64;

Query Match 75.0%; Score 36; DB 2; Length 213;
Best Local Similarity 71.4%; Pred. No. 53;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HDAPGYD 7
Db 98 HDAPLGF 104

RESULT 35
ID Q8J40 XENLA PRELIMINARY; PRT; 229 AA.
ID Q8J40 XENLA PRELIMINARY; PRT; 229 AA.
AC Q8J40 XENLA PRELIMINARY; PRT; 229 AA.
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Mitotic phosphoprotein 77 (fragment).
OS *Xenopus laevis* (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
OC Xenopodinae; Xenopus; Xenopus.
OX NCBI_TaxID=8355;

Best Local Similarity 75.0%; Score 36; DB 2; Length 229;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 2 DAPIGYD 8
Db 157 DSPGYD 163

RESULT 36
Q4PDF5 USTMA PRELIMINARY; PRT; 461 AA.
ID Q4PDF5 USTMA PRELIMINARY; PRT; 461 AA.
AC Q4PDF5 USTMA PRELIMINARY; PRT; 461 AA.
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Hypothetical protein.
GN ORFNames=OM01858.1;
OS *Ustilago maydis* 521.
OC Eukaryota; Fungi; Basidiomycota; Ustilaginomycetes;
OC Ustilaginomycetidae; Ustilaginales; Ustilaginaceae; Ustilago.
OX NCBI_TaxID=237631;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=521;
RA Birren B., Nisbaum C., Abebe A., Abouelleil A., Adekoya E.,
RA Alt-zahra M., Allen N., Allen T., An P., Anderson M., Anderson S.,
RA Archachl H., Amburster J., Bachantsang P., Baldwin C., Barry A.,
RA Bayul T., Biltshetyn B., Bloom T., Blye J., Boguslavsky L.,
RA Botovsky M., Boukhalter B., Brunache A., Butler J., Calixte N.,
RA Calvo S., Camarata J., Campo K., Chang J., Cheshtsang Y., Citroen M.,
RA Collimore A., Considine T., Cook A., Cooke P., Corum B., Cuomo C.,
RA David R., Dawoe T., Degray S., Dodge S., Dooley K., Dorje P.,
RA Dorjee K., Dorris L., Dufey N., Dupes A., Elkins T., Engels R.,
RA Erickson J., Farina A., Faro S., Ferreira P., Fischer H.,
RA Fitzgerald M., Foley K., Gage D., Galagan J., Geartig G., Gnerre S.,
RA Gnirke A., Goyette A., Graham J., Grandbois E., Gyaltsen K., Hafez N.,
RA Hagopian D., Hagoos B., Hall J., Hatcher B., Heller A., Higgins H.,
RA Honan T., Horn A., Houde N., Hughes L., Hulme W., Hubby B., Iliev I.,
RA Jaffe D., Jones C., Kamel M., Kamet A., Kanyaselski M., Karlsson E.,
RA Kells C., Kieu A., Kistner P., Kodira C., Kulbokas E., Labuttl K.,
RA Lama D., Landers T., Leiger J., Levine S., Lewis D., Lewis T.,
RA Lindblad-coh K., Liu X., Lokysang T., Lokysang Y., Lucien O.,
RA Lui A., Ma L.J., Mabbitt R., Macdonald J., Maclean C., Major J.,
RA Manning J., Marabelli R., Maru K., Matthews C., Mauceli E.,
RA McCarthy M., McDonough S., McGhee T., Meldrum J., Menus L.,
RA Mestrov J., Mihalev A., Minova T., Mikelsen T., Mlenga V., Moru K.,
RA Mozes J., Mulrain L., Munson G., Naylor J., Neves C., Nguyen C.,
RA Nguyen N., Nguyen T., Nicol R., Nielsen C., Nizari M., Norbu C.,
RA Norbu N., O'donnell P., Okoawo O., O'leary S., Omotoesho B.,
RA O'Neill K., Oman S., Parker S., Perrin D., Phunkhang P., Piquant B.,
RA Purcell S., Rachupka T., Ramasamy U., Rameau R., Ray V., Raymond C.,
RA Retta R., Richardson S., Rise C., Rodriguez J., Rogers J., Rogov P.,

RA Rutman M., Schupbach R., Seaman C., Settillalli S., Sharpe T.,
 RA Sheridan J., Shepa N., Sni J., Smirnov S., Smith C., Sougnuez C.,
 RA Spencer B., Stalker N., Strange-Thomann N., Stavropoulos S.,
 RA Stenson K., Stone C., Stone S., Stubbs M., Talamao J., Tchinga P.,
 RA Tenzing P., Testaye S., Theodore J., Thoulitsang Y., Topham K.,
 RA Toney S., Tsamila T., Tsomo N., Vallee D., Vassiliev H.,
 RA Venkataraman V., Vinsom J., Vo A., Wade C., Wang S., Mangchuk T.,
 RA Wangdi T., Whitaker C., Wilkinson J., Wu Y., Wyman D., Yadav S.,
 RA Yang S., Yang X., Yeager S., Yee E., Young G., Zainoun J., Zembeck L.,
 RA Zimmer A., Zody M., Lander E.;
 RT "The genome sequence of *Ustilago maydis*.";
 RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
 CC -1- CAUTION: The sequence shown here is derived from an
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.
 DR EMBL; AAC0100070; EAK82739.1; -; Genomic_DNA.
 DR InterPro; IPR005925; Agmatinase.
 DR InterPro; IPR006035; Arg_agsm_form.
 DR InterPro; IPR005924; Arginase.
 DR Pfam; PF00491; Arginase; 1.
 DR PRINTS; PR00116; ARGINASE.
 DR TIGRFAMs; TIGR01230; agmatinase; 1.
 DR PROSITE; PS00147; ARGINASE_1; UNKNOWN_1.
 DR PROSITE; PS00148; ARGINASE_2; UNKNOWN_1.
 DR PROSITE; PS01053; ARGINASE_3; 1.
 KW Hydrolase; Hypothetical protein; Manganase.
 SQ SEQUENCE 461 AA; 50026 MW; A664ADE84FA2706 CRC64;

Qy 1 HDAPIGD 8
 Db 312 HDASIGFD 319

Query Match 75.0%; Score 36; DB 2; Length 461;
 Best Local Similarity 75.0%; Pred. No. 1.2e+02;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

RESULT 37
 069531_ORYSA PRELIMINARY; PRT; 66 AA.
 ID 069531_ORYSA
 AC 069531;
 DT 25-OCT-2004 (TREMBLrel. 28, Created)
 DT 25-OCT-2004 (TREMBLrel. 28, Last sequence update)
 DT 25-OCT-2004 (TREMBLrel. 28, Last annotation update)
 DE Hypothetical protein OSCNB0058118.37.
 GN Name=OSUNBA0058118.37;
 OS Oryza sativa (Japonica cultivar-group).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Ehrhartoideae; Oryzaceae; Oryza.
 CC EMBL; AF002086; BAB16216.1; -; Genomic_DNA.
 CC NCBI_TaxID=39947;
 CC NCB1_TaxID=39947;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Sasaki T., Matsumoto T., Katayose Y.;
 RT "Oryza sativa nipponbare (GA3) genomic DNA, chromosome 7, BAC
 RT clone:OSUNBA0058118.";
 RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AP005125; BAB30915.1; -; Genomic_DNA.
 DR Gramene; Q69531; -;
 KW Hypothetical protein.
 SQ SEQUENCE 66 AA; 6970 MW; 48E4CA89A983ECD6 CRC64;

Qy 1 HDAPIG 6
 Db 13 HDAPIG 18

Query Match 72.9%; Score 35; DB 2; Length 66;
 Best Local Similarity 100.0%; Pred. No. 24;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 38
 Q9F5F3_AGRRH

ID Q9F5F3_AGRRH PRELIMINARY; PRT; 171 AA.
 AC Q9F5F3;
 DT 01-MAR-2001 (TREMBLrel. 16, Created)
 DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
 DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
 DE Rior197 protein.
 GN Name=rior197;
 OS Agrobacterium rhizogenes.
 OC plasmid pRi1724.
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
 OC Rhizobiaceae; Rhizobium/Agrobacterium group; Agrobacterium.
 CC NCBI_TaxID=359;
 CC NCB1_TaxID=359;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=MAFP03-01724;
 RA Moriguchi K., Nishida T., Maeda Y., Tanaka N., Yoshida K.;
 RT "Genome structure of R1 plasmid (1): Construction of linking library
 RT and physical map of pRi1724 in Japanese Agrobacterium.";
 RL Nucleic Acids Symp. Ser. 39:189-190(1998).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=MAFP03-01724;
 RA Moriguchi K., Nishida T., Maeda Y., Tanaka N., Yoshida K.;
 RT "Genome structure of R1 plasmid (1): Construction of linking library
 RT and physical map of pRi1724 in Japanese Agrobacterium.";
 RL Nucleic Acids Symp. Ser. 39:189-190(1998).
 RN [3]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=MAFP03-01724;
 RX PubMed=11273700; DOI=10.1006/jmbi.2001.4488;
 RA Moriguchi K., Maeda Y., Satou M., Harayama N.S.N., Kataoka M.,
 RA Tanaka N., Yoshida K.;
 RT "The complete nucleotide sequence of a plant root-inducing (Ri)
 RT plasmid indicates its chimeric structure and evolutionary relationship
 RT between tumor-inducing (Ti) and symbiotic (Sym) plasmids in
 RT Rhizobiaceae.";
 RL J. Mol. Biol. 307:771-784(2001).
 RN [4]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=MAFP03-01724;
 RX MEDLINE=20363091; PubMed=10907845;
 RA Moriguchi K., Maeda Y., Satou M., Kataoka M., Tanaka N., Yoshida K.;
 RT "Analysis of unique variable region of a plant root inducing plasmid,
 RT pRi1724, by the construction of its physical map and library.";
 RL DNA Res. 7:157-163(2000).
 DR EMBL; AP002086; BAB16216.1; -; Genomic_DNA.
 KW Plasmid.
 SQ SEQUENCE 171 AA; 18295 MW; 730160B1FDD0F52 CRC64;

Qy 2 DAPIGD 8
 Db 99 DGPVGD 105

Query Match 72.9%; Score 35; DB 2; Length 171;
 Best Local Similarity 71.4%; Pred. No. 67;
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

RESULT 39
 Q9LZG9_ARATH PRELIMINARY; PRT; 180 AA.
 ID Q9LZG9_ARATH
 AC Q9LZG9;
 DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
 DE Hypothetical protein T28A8_70.
 GN Name=T28A8_70;
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.

```

OX NCBI_TaxID=3702;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Punnett B., Boutry M., Goffeau A., Mewes H.W., Rudd S., Lemcke K.,
RA Mayer K.F.X., Quetier F., Salanoubat M.,
RL Submitted (MAR-2000) to the EMBL/Genbank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA EU Arabidopsis sequencing project;
RL Submitted (MAR-2000) to the EMBL/Genbank/DBJ databases.
DR EMBL; AL162691; CAB83150.1; -; Genomic_DNA.
DR PIR; T47414; T47414.
KM Hypothetical protein.
SQ SEQUENCE 180 AA; 19838 MW; 42A91B9998E18CFF CRC64;

Query Match 72.9%; Score 35; DB 2; Length 180;
Best Local Similarity 75.0%; Pred. No. 71;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 1 HDAPGYD 8
Db 38 HDIPGYD 45

RESULT 40
Q9R6J9_9RH1Z
ID Q9R6J9_9RH1Z PRELIMINARY; PRT; 199 AA.
AC Q9R6J9;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Tiorf60 protein.
GN Name=Tiorf60;
OS Agrobacterium tumefaciens.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Rhizobiaceae; Rhizobium/Agrobacterium group; Agrobacterium.
OX NCBI_TaxID=358;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=MAFF301001;
RA Hattori Y., Suzuki K., Ohta N., Uraji M., Katoh A., Yoshida K.;
RT "Genome structure of pTI-SAKURA (I): Strategy for DNA sequencing of a
RT Japanese cherry-Ti plasmid."
RL Nucleic Acids Symp. Ser. 37:159-160(1998).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=MAFF301001;
RA Ohta N., Suzuki K., Hattori Y., Uraji M., Katoh A., Yoshida K.;
RT "Genome structure of pTI-SAKURA (III): Characteristics of T-DNA."
RL Nucleic Acids Symp. Ser. 39:185-186(1998).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=MAFF301001;
RA Uraji M., Suzuki K., Ohta N., Hattori Y., Katoh A., Yoshida K.;
RT "Genome structure of pTI-SAKURA (IV): Characteristics of tra region."
RL Nucleic Acids Symp. Ser. 39:187-188(1998).
RN [4]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=MAFF301001;
RA Hattori Y., Suzuki K., Ohta N., Uraji M., Katoh A., Yoshida K.;
RT "Genome structure of pTI-SAKURA (V): Complete nucleotide sequence of
RT plasmid pTI-SAKURA's vir region in Agrobacterium tumefaciens."
RL Nucleic Acids Symp. Ser. 39:265-266(1998).
RN [5]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=MAFF301001;
RX MEDLINE=20184752; PubMed=10721727; DOI=10.1016/S0378-1119(99)00502-8;
RA Suzuki K., Hattori Y., Uraji M., Ohta N., Iwata K., Murata K.,
RA Katoh A., Yoshida K.;
RT "Complete nucleotide sequence of a plant tumor-inducing Ti plasmid."
RL Gene 242:331-336(2000).
RN [6]

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RP NUCLEOTIDE SEQUENCE.
RC STRAIN=MAFF301001;
RX MEDLINE=98193120; PubMed=9524202; DOI=10.1016/S0167-4781(97)00182-6;
RA Suzuki K., Ohta N., Hattori Y., Uraji M., Katoh A., Yoshida K.;
RT "Novel structural difference between nopaline- and octopine- type trbu
RT gene: construction of genetic and physical map and sequencing of
RT trb/traI and rep gene clusters of a new Ti plasmid pTI-SAKURA."
RL Blochim. Biophys. Acta 1396:1-7(1998).
DR EMBL; AB016260; BAA87685.1; -; Genomic_DNA.
KM Plasmid.
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Oy 2 DAPGYD 8
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Search completed: December 3, 2005, 23:42:54
 Job time : 232 secs

Pending Nucleic Acid and Pending Amino Acid database searches generate two sets of results each. The Pending databases have been split into two parts to reduce the amount of time required for their daily updates. This results in more machine time being available for processing searches. Searches run against the Nucleic Acid Pending database produce two sets of results, with the extensions **.rnpn** and **.rnpn**. Searches run against the Amino Acid Pending database produce two sets of results, with the extensions **.rapn** and **.rapn**.

Because they contain data that is confidential, the results of Pending database searches should not be left in the case .

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Curison k.
10/807553 Page 3
Seq. ID 2 w/ notes

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 3, 2005, 23:24:59 ; Search time 567 Seconds

(without alignments)
19.498 Million cell updates/sec

Title: US-10-807-553-2

Sequence: 1 HDAPIGYD 8

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Gapop 10.0 , Gapext 0.5

Searched: 7861189 seqs, 1381955077 residues

Total number of hits satisfying chosen parameters: 7861189

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
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Listing first 100 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	48	100.0	8	1 PCT-US02-11754-2	Sequence 2, Appl1
3	48	100.0	8	30 US-10-007-363-2	Sequence 2, Appl1
4	48	100.0	8	38 US-10-807-553-2	Sequence 2, Appl1
5	48	100.0	8	40 US-11-011-557-3	Sequence 3, Appl1
6	48	100.0	30	40 US-11-011-557-93	Sequence 93, Appl1
7	48	100.0	123	46 US-60-208-965-244	Sequence 244, Appl1
8	48	100.0	125	46 US-60-233-606-114	Sequence 114, Appl1
9	48	100.0	231	39 US-10-932-349-1539	Sequence 1539, Appl1
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ALIGNMENTS

RESULT 1
PCT-US01-51600-2
Sequence 2, Application PC/TUS0151600
GENERAL INFORMATION:
APPLICANT: The Board of Trustees of the Leland
APPLICANT: Stanford Junior University
TITLE OF INVENTION: pseudo-epsilon RACK Peptide Composition
TITLE OF INVENTION: and Method for Protection Against Tissue Damage Due to
TITLE OF INVENTION: Ischemia
FILE REFERENCE: 58600-8209.WO00
CURRENT APPLICATION NUMBER: PCT/US01/51600
CURRENT FILING DATE: 2001-11-09
PRIOR APPLICATION NUMBER: US 60/247,830
PRIOR FILING DATE: 2000-11-10
NUMBER OF SEQ ID NOS: 18
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 2
LENGTH: 8
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: pseudo-epsilon RACK octapeptide
PCT-US01-51600-2

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Best Local Similarity 100.0%; Pred. No. 7.2e+06;
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Sequence 2, Application PC/TUS0211754
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APPLICANT: The Board of Trustees of the Leland
APPLICANT: Stanford Junior University
TITLE OF INVENTION: pseudo-epsilon RACK Peptide Composition
TITLE OF INVENTION: and Method for Protection Against Tissue Damage Due to
TITLE OF INVENTION: Ischemia
FILE REFERENCE: 58600-8209.WO00
CURRENT APPLICATION NUMBER: PCT/US02/11754
CURRENT FILING DATE: 2002-04-12
PRIOR APPLICATION NUMBER: US 60/247,830
PRIOR FILING DATE: 2000-11-10
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SOFTWARE: FastSeq for Windows Version 4.0
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GENERAL INFORMATION:
APPLICANT: Mochly-Rosen, Daria
TITLE OF INVENTION: pseudo-epsilon RACK Peptide Composition
TITLE OF INVENTION: and Method for Protection Against Tissue Damage Due to
TITLE OF INVENTION: Ischemia
FILE REFERENCE: 58600-8209.US00
CURRENT APPLICATION NUMBER: US/10/007,363
CURRENT FILING DATE: 2002-11-09
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GENERAL INFORMATION:
APPLICANT: Mochly-Rosen, Daria
TITLE OF INVENTION: pseudo-epsilon RACK Peptide Composition
TITLE OF INVENTION: and Method for Protection Against Tissue Damage Due to
TITLE OF INVENTION: Ischemia
FILE REFERENCE: 58600-8209.US00
CURRENT APPLICATION NUMBER: US/10/807,553
CURRENT FILING DATE: 2004-03-22
PRIOR APPLICATION NUMBER: US/10/007,363
PRIOR FILING DATE: 2001-11-09
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PRIOR FILING DATE: 2000-11-10
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US-10-807-553-2

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Sequence 3, Application US/11011557
GENERAL INFORMATION:
APPLICANT: Mochly-Rosen, Daria
APPLICANT: Chen, Leon E.
TITLE OF INVENTION: Isozyme-Specific Antagonists of Protein Kinase C
FILE REFERENCE: 58600-8212.US00
CURRENT APPLICATION NUMBER: US/11/011,557
CURRENT FILING DATE: 2004-12-13
PRIOR APPLICATION NUMBER: 60/529,223
PRIOR FILING DATE: 2003-12-11
NUMBER OF SEQ ID NOS: 97
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TYPE: PRT
ORGANISM: Homo sapiens
US-11-011-557-3

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US-11-011-557-93
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GENERAL INFORMATION:
APPLICANT: Mochly-Rosen, Daria
APPLICANT: Chen, Leon E.
TITLE OF INVENTION: Isozyme-Specific Antagonists of Protein Kinase C
FILE REFERENCE: 58600-8212.US00

CURRENT APPLICATION NUMBER: US/11/011,557
CURRENT FILING DATE: 2004-12-13
PRIOR APPLICATION NUMBER: 60/529,223
PRIOR FILING DATE: 2003-12-11
NUMBER OF SEQ ID NOS: 97
SOFTWARE: PatentIn version 3.3
SEQ ID NO 93
LENGTH: 30
TYPE: PRT
ORGANISM: Homo sapiens
US-11-011-557-93

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Db 15 HDAPIGYD 22

RESULT 7
US-60-208-965-244
Sequence 244, Application US/60208965
GENERAL INFORMATION:
APPLICANT: Beasley, Ellen
TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS OF THE
TITLE OF INVENTION: SER/THR AND TYR FAMILY OF KINASES, NUCLEIC ACID MOLECULES
FILE REFERENCE: CL000639
CURRENT APPLICATION NUMBER: US/60/208,965
CURRENT FILING DATE: 2000-06-02
NUMBER OF SEQ ID NOS: 244
SOFTWARE: FastSeq for Windows Version 4.0
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LENGTH: 123
TYPE: PRT
ORGANISM: HUMAN
US-60-208-965-244

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Db 84 HDAPIGYD 91

RESULT 8
US-60-233-606-114
Sequence 114, Application US/60233606
GENERAL INFORMATION:
APPLICANT: Beasley, Ellen
TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS OF THE
TITLE OF INVENTION: SER/THR AND TYR FAMILY OF KINASES, NUCLEIC ACID MOLECULES
FILE REFERENCE: CL000821
CURRENT APPLICATION NUMBER: US/60/233,606
CURRENT FILING DATE: 2000-09-18
NUMBER OF SEQ ID NOS: 174
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 114
LENGTH: 125
TYPE: PRT
ORGANISM: HUMAN
US-60-233-606-114

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Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 HDAPIGYD 8

Db 71 HDAPIGYD 78

RESULT 9
US-10-932-349-1539

/ Sequence 1539, Application US/10932349
/ GENERAL INFORMATION:
/ APPLICANT: CARGILL, Michele
/ TITLE OF INVENTION: POLYMORPHISMS IN NUCLEIC ACID MOLECULES
/ TITLE OF INVENTION: ENCODING HUMAN KINASE PROTEINS, METHODS OF DETECTION AND
/ FILE REFERENCE: CLO01483
/ CURRENT APPLICATION NUMBER: US/10/932,349
/ CURRENT FILING DATE: 2004-09-02
/ NUMBER OF SEQ ID NOS: 123188
/ SOFTWARE: FASTSEQ for Windows Version 4.0
/ SEQ ID NO: 1539
/ LENGTH: 231
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-932-349-1539

Query Match 100.0%; Score 48; DB 39; Length 231;
Best Local Similarity 100.0%; Pred. No. 2.8;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HDAPIGYD 8
Db 85 HDAPIGYD 92

RESULT 10
US-60-500-337-1539

/ Sequence 1539, Application US/60500337
/ GENERAL INFORMATION:
/ APPLICANT: CARGILL, Michele
/ TITLE OF INVENTION: POLYMORPHISMS IN NUCLEIC ACID MOLECULES
/ TITLE OF INVENTION: ENCODING HUMAN KINASE PROTEINS, METHODS OF DETECTION AND
/ FILE REFERENCE: CLO01483
/ CURRENT APPLICATION NUMBER: US/60/500,337
/ CURRENT FILING DATE: 2003-09-05
/ NUMBER OF SEQ ID NOS: 123188
/ SOFTWARE: FASTSEQ for Windows Version 4.0
/ SEQ ID NO: 1539
/ LENGTH: 231
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-60-500-337-1539

Query Match 100.0%; Score 48; DB 49; Length 231;
Best Local Similarity 100.0%; Pred. No. 2.8;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HDAPIGYD 8
Db 85 HDAPIGYD 92

RESULT 11
US-09-791-537-106215

/ Sequence 106215, Application US/09791537
/ GENERAL INFORMATION:
/ APPLICANT: Bionomix, Inc.
/ APPLICANT: Debe, Derek
/ APPLICANT: Danzer, Joseph
/ TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMB
/ TITLE OF INVENTION: METHODS OF USE THEREOF
/ FILE REFERENCE: 261/210
/ CURRENT APPLICATION NUMBER: US/09/791,537
/ CURRENT FILING DATE: 2001-02-22
/ NUMBER OF SEQ ID NOS: 153055

/ SOFTWARE: PatentIn version 3.0
/ SEQ ID NO: 106215
/ LENGTH: 736
/ TYPE: PRT
/ ORGANISM: Oryctolagus cuniculus
US-09-791-537-106215

Query Match 100.0%; Score 48; DB 27; Length 736;
Best Local Similarity 100.0%; Pred. No. 9.2;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HDAPIGYD 8
Db 85 HDAPIGYD 92

RESULT 12
US-09-791-537-108607

/ Sequence 108607, Application US/09791537
/ GENERAL INFORMATION:
/ APPLICANT: Bionomix, Inc.
/ APPLICANT: Debe, Derek
/ APPLICANT: Danzer, Joseph
/ TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMB
/ TITLE OF INVENTION: METHODS OF USE THEREOF
/ FILE REFERENCE: 261/210
/ CURRENT APPLICATION NUMBER: US/09/791,537
/ CURRENT FILING DATE: 2001-02-22
/ NUMBER OF SEQ ID NOS: 153055
/ SOFTWARE: PatentIn version 3.0
/ SEQ ID NO: 108607
/ LENGTH: 736
/ TYPE: PRT
/ ORGANISM: Oryctolagus cuniculus
US-09-791-537-108607

Query Match 100.0%; Score 48; DB 27; Length 736;
Best Local Similarity 100.0%; Pred. No. 9.2;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HDAPIGYD 8
Db 85 HDAPIGYD 92

RESULT 13
PCT-US02-01048-2

/ Sequence 2, Application PC/TUS0201048
/ GENERAL INFORMATION:
/ APPLICANT: EXLIXIS, INC.
/ TITLE OF INVENTION: Modulating Insulin Receptor Signaling
/ FILE REFERENCE: EX02-001C-PC
/ CURRENT APPLICATION NUMBER: PCT/US02/01048
/ CURRENT FILING DATE: 2002-01-11
/ Prior Application removed - See File Wrapper or Palm
/ NUMBER OF SEQ ID NOS: 76
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO: 2
/ LENGTH: 737
/ TYPE: PRT
/ ORGANISM: Homo sapiens
PCT-US02-01048-2

Query Match 100.0%; Score 48; DB 1; Length 737;
Best Local Similarity 100.0%; Pred. No. 9.2;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HDAPIGYD 8
Db 85 HDAPIGYD 92

RESULT 14

```

US-07-821-714-2
: Sequence 2, Application US/07821714
: GENERAL INFORMATION:
: APPLICANT: Basca, Patricia V.
: APPLICANT: Burns, David J.
: TITLE OF INVENTION: Epsilon Isoenzyme of Protein Kinase C
: NUMBER OF SEQUENCES: 13
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & Norris
: STREET: 1 Liberty Place, 46th Floor
: CITY: Philadelphia
: STATE: PA
: COUNTRY: USA
: ZIP: 19103
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/07/821,714
: FILING DATE: 19920114
: CLASSIFICATION: 435
: ATTORNEY/AGENT INFORMATION:
: NAME: Hohenschutz, Liza D.
: REGISTRATION NUMBER: 33,712
: REFERENCE/DOCKET NUMBER: SPNX-0010
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (215) 568-3100
: TELEFAX: (215) 568-3439
: INFORMATION FOR SEQ ID NO: 2:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 737 amino acids
: TYPE: AMINO ACID
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: US-07-821-714-2

```

```

Query Match      100.0%; Score 48; DB 8; Length 737;
Best Local Similarity 100.0%; Pred. No. 9.2;
Matches      8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      1 HDAPIGYD 8
Db      85 HDAPIGYD 92

```

```

RESULT 15
US-07-821-714-4
: Sequence 4, Application US/07821714
: GENERAL INFORMATION:
: APPLICANT: Basca, Patricia V.
: APPLICANT: Burns, David J.
: TITLE OF INVENTION: Epsilon Isoenzyme of Protein Kinase C
: NUMBER OF SEQUENCES: 13
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & Norris
: STREET: 1 Liberty Place, 46th Floor
: CITY: Philadelphia
: STATE: PA
: COUNTRY: USA
: ZIP: 19103
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/07/821,714
: FILING DATE: 19920114
: CLASSIFICATION: 435
: ATTORNEY/AGENT INFORMATION:
: NAME: Hohenschutz, Liza D.

```

```

: REGISTRATION NUMBER: 33,712
: REFERENCE/DOCKET NUMBER: SPNX-0010
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (215) 568-3100
: TELEFAX: (215) 568-3439
: INFORMATION FOR SEQ ID NO: 4:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 737 amino acids
: TYPE: AMINO ACID
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: US-07-821-714-4

```

```

Query Match      100.0%; Score 48; DB 8; Length 737;
Best Local Similarity 100.0%; Pred. No. 9.2;
Matches      8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      1 HDAPIGYD 8
Db      85 HDAPIGYD 92

```

```

RESULT 16
US-08-087-341-2
: Sequence 2, Application US/08087341
: GENERAL INFORMATION:
: APPLICANT: Basca, Patricia V.
: APPLICANT: Burns, David J.
: TITLE OF INVENTION: Epsilon Isoenzyme of Protein Kinase C
: NUMBER OF SEQUENCES: 13
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & Norris
: STREET: 1 Liberty Place, 46th Floor
: CITY: Philadelphia
: STATE: PA
: COUNTRY: USA
: ZIP: 19103
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/087,341
: FILING DATE:
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US/07/821,714
: FILING DATE:
: ATTORNEY/AGENT INFORMATION:
: NAME: Hohenschutz, Liza D.
: REGISTRATION NUMBER: 33,712
: REFERENCE/DOCKET NUMBER: SPNX-0010
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (215) 568-3100
: TELEFAX: (215) 568-3439
: INFORMATION FOR SEQ ID NO: 2:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 737 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: US-08-087-341-2

```

```

Query Match      100.0%; Score 48; DB 10; Length 737;
Best Local Similarity 100.0%; Pred. No. 9.2;
Matches      8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      1 HDAPIGYD 8
Db      85 HDAPIGYD 92

```

RESULT 17
US-08-087-341-4
Sequence 4, Application US/08087341
GENERAL INFORMATION:
APPLICANT: Basta, Patricia V.
APPLICANT: Burns, David J.
TITLE OF INVENTION: Epsilon Isoenzyme of Protein Kinase C
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & Norris
STREET: 1 Liberty Place, 46th Floor
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/087,341
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/821,714
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Hohenschutz, Liza D.
REGISTRATION NUMBER: 33,712
REFERENCE/DOCKET NUMBER: SPNX-0010
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-3100
TELEFAX: (215) 568-3439
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 737 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-087-341-4

Query Match 100.0%; Score 48; DB 10; Length 737;
Best Local Similarity 100.0%; Pred. No. 9.2;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HDAPIGYD 8
DB 85 HDAPIGYD 92

RESULT 18
US-08-087-341A-2
Sequence 2, Application US/08087341A
GENERAL INFORMATION:
APPLICANT: Basta, Patricia V.
APPLICANT: Burns, David J.
TITLE OF INVENTION: Epsilon Isoenzyme of Protein Kinase C
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & Norris
STREET: 1 Liberty Place, 46th Floor
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/087,341A

FILING DATE: 02-JUL-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/821,714
FILING DATE: 14-JAN-1992
ATTORNEY/AGENT INFORMATION:
NAME: Deluca, Mark
REGISTRATION NUMBER: 33,229
REFERENCE/DOCKET NUMBER: SPNX-0317
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-3100
TELEFAX: (215) 568-3439
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 737 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-087-341A-2

Query Match 100.0%; Score 48; DB 10; Length 737;
Best Local Similarity 100.0%; Pred. No. 9.2;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HDAPIGYD 8
DB 85 HDAPIGYD 92

RESULT 19
US-08-087-341A-4
Sequence 4, Application US/08087341A
GENERAL INFORMATION:
APPLICANT: Basta, Patricia V.
APPLICANT: Burns, David J.
TITLE OF INVENTION: Epsilon Isoenzyme of Protein Kinase C
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & Norris
STREET: 1 Liberty Place, 46th Floor
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/087,341A
FILING DATE: 02-JUL-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/821,714
FILING DATE: 14-JAN-1992
ATTORNEY/AGENT INFORMATION:
NAME: Deluca, Mark
REGISTRATION NUMBER: 33,229
REFERENCE/DOCKET NUMBER: SPNX-0317
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-3100
TELEFAX: (215) 568-3439
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 737 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-087-341A-4

Query Match 100.0%; Score 48; DB 10; Length 737;
Best Local Similarity 100.0%; Pred. No. 9.2;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HDAPIGYD 8
|||
Db 85 HDAPIGYD 92

RESULT 20
US-09-791-537-27401
; Sequence 27401, Application US/09791537
; GENERAL INFORMATION:
; APPLICANT: Bionomix, Inc.
; APPLICANT: Debe, Derek
; APPLICANT: Danzer, Joseph
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBERS
; FILE REFERENCE: 261/210
; CURRENT APPLICATION NUMBER: US/09/791,537
; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 153055
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 27401
; LENGTH: 737
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-791-537-27401

Query Match
Best Local Similarity 100.0%; Score 48; DB 27; Length 737;
Pred. No. 9.2;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HDAPIGYD 8
|||
Db 85 HDAPIGYD 92

RESULT 21
US-09-791-537-35026
; Sequence 35026, Application US/09791537
; GENERAL INFORMATION:
; APPLICANT: Bionomix, Inc.
; APPLICANT: Debe, Derek
; APPLICANT: Danzer, Joseph
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBERS
; FILE REFERENCE: 261/210
; CURRENT APPLICATION NUMBER: US/09/791,537
; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 153055
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 35026
; LENGTH: 737
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-791-537-35026

Query Match
Best Local Similarity 100.0%; Score 48; DB 27; Length 737;
Pred. No. 9.2;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HDAPIGYD 8
|||
Db 85 HDAPIGYD 92

RESULT 22
US-09-791-537-106216
; Sequence 106216, Application US/09791537
; GENERAL INFORMATION:
; APPLICANT: Bionomix, Inc.
; APPLICANT: Debe, Derek
; APPLICANT: Danzer, Joseph
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBERS

; TITLE OF INVENTION: METHODS OF USE THEREOF
; FILE REFERENCE: 261/210
; CURRENT APPLICATION NUMBER: US/09/791,537
; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 153055
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 106216
; LENGTH: 737
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-09-791-537-106216

Query Match
Best Local Similarity 100.0%; Score 48; DB 27; Length 737;
Pred. No. 9.2;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HDAPIGYD 8
|||
Db 85 HDAPIGYD 92

RESULT 23
US-10-170-205E-13606
; Sequence 13606, Application US/10170205E
; GENERAL INFORMATION:
; APPLICANT: ADAMS, Mark
; TITLE OF INVENTION: DEVICES, SUCH AS ARRAYS, COMPRISED OF HUMAN PROTEINS OR PROTEIN
; FILE REFERENCE: CL001381
; CURRENT APPLICATION NUMBER: US/10/170,205E
; CURRENT FILING DATE: 2002-06-13
; NUMBER OF SEQ ID NOS: 40312
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 13606
; LENGTH: 737
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-170-205E-13606

Query Match
Best Local Similarity 100.0%; Score 48; DB 31; Length 737;
Pred. No. 9.2;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HDAPIGYD 8
|||
Db 85 HDAPIGYD 92

RESULT 24
US-10-219-051B-3331
; Sequence 3331, Application US/10219051B
; GENERAL INFORMATION:
; APPLICANT: The General Hospital Corporation doing business as Massachusetts General
; APPLICANT: Hospital / Bayer AG
; TITLE OF INVENTION: Nucleotide sequences involved in pain
; FILE REFERENCE: Lea 35693 Foreign Countries
; CURRENT APPLICATION NUMBER: US/10/219,051B
; CURRENT FILING DATE: 2003-05-09
; PRIOR APPLICATION NUMBER: US 60/312,147
; PRIOR FILING DATE: 2001-08-14
; PRIOR APPLICATION NUMBER: US 60/346,382
; PRIOR FILING DATE: 2001-11-01
; PRIOR APPLICATION NUMBER: US 60/333,347
; PRIOR FILING DATE: 2001-11-26
; NUMBER OF SEQ ID NOS: 14715
; SOFTWARE: Perl script
; SEQ ID NO 3331
; LENGTH: 737
; TYPE: PRT
; ORGANISM: Homo sapiens
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: SWISS-Prot / Q02156
; DATABASE ENTRY DATE: 2002-06-15

US-10-219-051B-3331

Query Match 100.0%; Score 48; DB 32; Length 737;
Best Local Similarity 100.0%; Pred. No. 9.2;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HDAPIGYD 8
Db 85 HDAPIGYD 92

RESULT 25

US-10-219-051B-3389
; Sequence 3389, Application US/10219051B
; GENERAL INFORMATION:
; APPLICANT: The General Hospital Corporation doing business as Massachusetts General
; TITLE OF INVENTION: Nucleotide sequences involved in pain
; FILE REFERENCE: Lea 35693 Foreign Countries
; CURRENT FILING DATE: 2003-05-09
; PRIOR FILING DATE: 2001-08-14
; PRIOR APPLICATION NUMBER: US 60/346,382
; PRIOR FILING DATE: 2001-11-01
; PRIOR APPLICATION NUMBER: US 60/333,347
; PRIOR FILING DATE: 2001-11-26
; NUMBER OF SEQ ID NOS: 14715
; SOFTWARE: Perl script
; SEQ ID NO 3389
; LENGTH: 737
; TYPE: PRT
; ORGANISM: Rattus norvegicus
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: SWISS-Prot / AAA41872
; DATABASE ENTRY DATE: 1999-07-15
US-10-219-051B-3389

Query Match 100.0%; Score 48; DB 32; Length 737;
Best Local Similarity 100.0%; Pred. No. 9.2;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HDAPIGYD 8
Db 85 HDAPIGYD 92

RESULT 26

US-10-219-051B-3391
; Sequence 3391, Application US/10219051B
; GENERAL INFORMATION:
; APPLICANT: The General Hospital Corporation doing business as Massachusetts General
; TITLE OF INVENTION: Nucleotide sequences involved in pain
; FILE REFERENCE: Lea 35693 Foreign Countries
; CURRENT FILING DATE: 2003-05-09
; PRIOR FILING DATE: 2001-08-14
; PRIOR APPLICATION NUMBER: US 60/346,382
; PRIOR FILING DATE: 2001-11-01
; PRIOR APPLICATION NUMBER: US 60/333,347
; PRIOR FILING DATE: 2001-11-26
; NUMBER OF SEQ ID NOS: 14715
; SOFTWARE: Perl script
; SEQ ID NO 3391
; LENGTH: 737
; TYPE: PRT
; ORGANISM: Homo sapiens
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: SWISS-Prot / Q02156
; DATABASE ENTRY DATE: 2002-06-15
US-10-219-051B-3391

Query Match 100.0%; Score 48; DB 32; Length 737;
Best Local Similarity 100.0%; Pred. No. 9.2;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HDAPIGYD 8
Db 85 HDAPIGYD 92

RESULT 27

US-10-219-051B-3393
; Sequence 3393, Application US/10219051B
; GENERAL INFORMATION:
; APPLICANT: The General Hospital Corporation doing business as Massachusetts General
; TITLE OF INVENTION: Nucleotide sequences involved in pain
; FILE REFERENCE: Lea 35693 Foreign Countries
; CURRENT FILING DATE: 2003-05-09
; PRIOR FILING DATE: 2001-08-14
; PRIOR APPLICATION NUMBER: US 60/346,382
; PRIOR FILING DATE: 2001-11-01
; PRIOR APPLICATION NUMBER: US 60/333,347
; PRIOR FILING DATE: 2001-11-26
; NUMBER OF SEQ ID NOS: 14715
; SOFTWARE: Perl script
; SEQ ID NO 3393
; LENGTH: 737
; TYPE: PRT
; ORGANISM: Rattus norvegicus
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: SWISS-Prot / AAA41872
; DATABASE ENTRY DATE: 1999-07-15
US-10-219-051B-3393

Query Match 100.0%; Score 48; DB 32; Length 737;
Best Local Similarity 100.0%; Pred. No. 9.2;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HDAPIGYD 8
Db 85 HDAPIGYD 92

RESULT 28

US-10-219-051B-3395
; Sequence 3395, Application US/10219051B
; GENERAL INFORMATION:
; APPLICANT: The General Hospital Corporation doing business as Massachusetts General
; TITLE OF INVENTION: Nucleotide sequences involved in pain
; FILE REFERENCE: Lea 35693 Foreign Countries
; CURRENT FILING DATE: 2003-05-09
; PRIOR FILING DATE: 2001-08-14
; PRIOR APPLICATION NUMBER: US 60/346,382
; PRIOR FILING DATE: 2001-11-01
; PRIOR APPLICATION NUMBER: US 60/333,347
; PRIOR FILING DATE: 2001-11-26
; NUMBER OF SEQ ID NOS: 14715
; SOFTWARE: Perl script
; SEQ ID NO 3395
; LENGTH: 737
; TYPE: PRT
; ORGANISM: Homo sapiens
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: SWISS-Prot / Q02156
; DATABASE ENTRY DATE: 2002-06-15
US-10-219-051B-3395

Query Match 100.0%; Score 48; DB 32; Length 737;
Best Local Similarity 100.0%; Pred. No. 9.2;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 HDAPIGYD 8
Db 85 HDAPIGYD 92

RESULT 29
US-10-219-051B-3397
; Sequence 3397, Application US/10219051B
; GENERAL INFORMATION:
; APPLICANT: The General Hospital Corporation doing business as Massachusetts General
; APPLICANT: Hospital / Bayer AG
; TITLE OF INVENTION: Nucleotide sequences involved in pain
; FILE REFERENCE: Lea 35693 Foreign Countries
; CURRENT APPLICATION NUMBER: US/10/219, 051B
; PRIOR FILING DATE: 2003-05-09
; PRIOR APPLICATION NUMBER: US 60/312,147
; PRIOR FILING DATE: 2001-08-14
; PRIOR APPLICATION NUMBER: US 60/346,382
; PRIOR FILING DATE: 2001-11-01
; PRIOR APPLICATION NUMBER: US 60/333,347
; PRIOR FILING DATE: 2001-11-26
; NUMBER OF SEQ ID NOS: 14715
; SOFTWARE: Perl script
; SEQ ID NO 3397
; LENGTH: 737
; TYPE: PRT
; ORGANISM: Rattus norvegicus
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: SWISS-Prot / AAA41872
; DATABASE ENTRY DATE: 1999-07-15
US-10-219-051B-3397

Query Match 100.0%; Score 48; DB 32; Length 737;
Best Local Similarity 100.0%; Pred. No. 9.2;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HDAPIGYD 8
Db 85 HDAPIGYD 92

RESULT 30
US-10-219-051B-3399
; Sequence 3399, Application US/10219051B
; GENERAL INFORMATION:
; APPLICANT: The General Hospital Corporation doing business as Massachusetts General
; APPLICANT: Hospital / Bayer AG
; TITLE OF INVENTION: Nucleotide sequences involved in pain
; FILE REFERENCE: Lea 35693 Foreign Countries
; CURRENT APPLICATION NUMBER: US/10/219, 051B
; PRIOR FILING DATE: 2003-05-09
; PRIOR APPLICATION NUMBER: US 60/312,147
; PRIOR FILING DATE: 2001-08-14
; PRIOR APPLICATION NUMBER: US 60/346,382
; PRIOR FILING DATE: 2001-11-01
; PRIOR APPLICATION NUMBER: US 60/333,347
; PRIOR FILING DATE: 2001-11-26
; NUMBER OF SEQ ID NOS: 14715
; SOFTWARE: Perl script
; SEQ ID NO 3399
; LENGTH: 737
; TYPE: PRT
; ORGANISM: Homo sapiens
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: SWISS-Prot / Q02156
; DATABASE ENTRY DATE: 2002-06-15
US-10-219-051B-3399

Query Match 100.0%; Score 48; DB 32; Length 737;

Best Local Similarity 100.0%; Pred. No. 9.2;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 HDAPIGYD 8
Db 85 HDAPIGYD 92

RESULT 31
US-10-219-051B-3401
; Sequence 3401, Application US/10219051B
; GENERAL INFORMATION:
; APPLICANT: The General Hospital Corporation doing business as Massachusetts General
; APPLICANT: Hospital / Bayer AG
; TITLE OF INVENTION: Nucleotide sequences involved in pain
; FILE REFERENCE: Lea 35693 Foreign Countries
; CURRENT APPLICATION NUMBER: US/10/219, 051B
; PRIOR FILING DATE: 2003-05-09
; PRIOR APPLICATION NUMBER: US 60/312,147
; PRIOR FILING DATE: 2001-08-14
; PRIOR APPLICATION NUMBER: US 60/346,382
; PRIOR FILING DATE: 2001-11-01
; PRIOR APPLICATION NUMBER: US 60/333,347
; PRIOR FILING DATE: 2001-11-26
; NUMBER OF SEQ ID NOS: 14715
; SOFTWARE: Perl script
; SEQ ID NO 3401
; LENGTH: 737
; TYPE: PRT
; ORGANISM: Rattus norvegicus
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: SWISS-Prot / AAA41872
; DATABASE ENTRY DATE: 1999-07-15
US-10-219-051B-3401

Query Match 100.0%; Score 48; DB 32; Length 737;
Best Local Similarity 100.0%; Pred. No. 9.2;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HDAPIGYD 8
Db 85 HDAPIGYD 92

RESULT 32
US-10-219-051B-3403
; Sequence 3403, Application US/10219051B
; GENERAL INFORMATION:
; APPLICANT: The General Hospital Corporation doing business as Massachusetts General
; APPLICANT: Hospital / Bayer AG
; TITLE OF INVENTION: Nucleotide sequences involved in pain
; FILE REFERENCE: Lea 35693 Foreign Countries
; CURRENT APPLICATION NUMBER: US/10/219, 051B
; PRIOR FILING DATE: 2003-05-09
; PRIOR APPLICATION NUMBER: US 60/312,147
; PRIOR FILING DATE: 2001-08-14
; PRIOR APPLICATION NUMBER: US 60/346,382
; PRIOR FILING DATE: 2001-11-01
; PRIOR APPLICATION NUMBER: US 60/333,347
; PRIOR FILING DATE: 2001-11-26
; NUMBER OF SEQ ID NOS: 14715
; SOFTWARE: Perl script
; SEQ ID NO 3403
; LENGTH: 737
; TYPE: PRT
; ORGANISM: Homo sapiens
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: SWISS-Prot / Q02156
; DATABASE ENTRY DATE: 2002-06-15
US-10-219-051B-3403

Query Match 100.0%; Score 48; DB 32; Length 737;
Best Local Similarity 100.0%; Pred. No. 9.2;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 HDAPIGYD 8
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Db 85 HDAPIGYD 92

RESULT 33
US-10-219-051B-4226
; Sequence 4226, Application US/10219051B
; GENERAL INFORMATION:
; APPLICANT: The General Hospital Corporation doing business as Massachusetts General
; APPLICANT: Hospital / Bayer AG
; TITLE OF INVENTION: Nucleotide sequences involved in pain
; FILE REFERENCE: Lea 35693 Foreign Countries
; CURRENT FILING DATE: 2003-05-09
; PRIOR APPLICATION NUMBER: US 60/312,147
; PRIOR FILING DATE: 2001-08-14
; PRIOR APPLICATION NUMBER: US 60/346,382
; PRIOR FILING DATE: 2001-11-01
; PRIOR APPLICATION NUMBER: US 60/333,347
; PRIOR FILING DATE: 2001-11-26
; NUMBER OF SEQ ID NOS: 14715
; SOFTWARE: Perl script
; SEQ ID NO 4226
; LENGTH: 737
; TYPE: PRT
; ORGANISM: Rattus norvegicus
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: SWISS-Prot / KIRTC
; DATABASE ENTRY DATE: 1999-07-15
US-10-219-051B-4226

Query Match 100.0%; Score 48; DB 32; Length 737;
Best Local Similarity 100.0%; Pred. No. 9.2;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HDAPIGYD 8
|||
Db 85 HDAPIGYD 92

RESULT 34
US-10-219-051B-4228
; Sequence 4228, Application US/10219051B
; GENERAL INFORMATION:
; APPLICANT: The General Hospital Corporation doing business as Massachusetts General
; APPLICANT: Hospital / Bayer AG
; TITLE OF INVENTION: Nucleotide sequences involved in pain
; FILE REFERENCE: Lea 35693 Foreign Countries
; CURRENT FILING DATE: 2003-05-09
; PRIOR APPLICATION NUMBER: US 60/312,147
; PRIOR FILING DATE: 2001-08-14
; PRIOR APPLICATION NUMBER: US 60/346,382
; PRIOR FILING DATE: 2001-11-01
; PRIOR APPLICATION NUMBER: US 60/333,347
; PRIOR FILING DATE: 2001-11-26
; NUMBER OF SEQ ID NOS: 14715
; SOFTWARE: Perl script
; SEQ ID NO 4228
; LENGTH: 737
; TYPE: PRT
; ORGANISM: Homo sapiens
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: SWISS-Prot / Q02156
; DATABASE ENTRY DATE: 2002-06-15
US-10-219-051B-4228

Query Match 100.0%; Score 48; DB 32; Length 737;
Best Local Similarity 100.0%; Pred. No. 9.2;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HDAPIGYD 8
|||
Db 85 HDAPIGYD 92

RESULT 35
US-10-307-700-24
; Sequence 24, Application US/10307700
; GENERAL INFORMATION:
; APPLICANT: Gonzalez-Zulueta, Mirella
; APPLICANT: Chin, Daniel J.
; APPLICANT: Wilson, Riche
; APPLICANT: McFarland, K.C.
; APPLICANT: Melcher, Thorsten
; APPLICANT: Wleloch, Tadeusz
; TITLE OF INVENTION: Ischemia Associated Genes
; FILE REFERENCE: AGYT-001
; CURRENT APPLICATION NUMBER: US/10/307,700
; CURRENT FILING DATE: 2002-12-02
; PRIOR APPLICATION NUMBER: 60/334,973
; PRIOR FILING DATE: 2001-11-30
; PRIOR APPLICATION NUMBER: 60/334,985
; PRIOR FILING DATE: 2001-11-30
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 24
; LENGTH: 737
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-307-700-24

Query Match 100.0%; Score 48; DB 33; Length 737;
Best Local Similarity 100.0%; Pred. No. 9.2;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HDAPIGYD 8
|||
Db 85 HDAPIGYD 92

RESULT 36
US-10-466-162-2
; Sequence 2, Application US/10466162
; GENERAL INFORMATION:
; APPLICANT: EXELIXIS, INC.
; TITLE OF INVENTION: Modulating Insulin Receptor Signaling
; FILE REFERENCE: EX02-001C-PC
; CURRENT FILING DATE: 2003-07-11
; PRIOR APPLICATION NUMBER: US 60/261,335
; PRIOR FILING DATE: 2001-01-12
; PRIOR APPLICATION NUMBER: US 60/261,694
; PRIOR FILING DATE: 2001-01-12
; PRIOR APPLICATION NUMBER: US 60/261,532
; PRIOR FILING DATE: 2001-01-12
; PRIOR APPLICATION NUMBER: US 60/261,361
; PRIOR FILING DATE: 2001-01-12
; PRIOR APPLICATION NUMBER: US 60/261,531
; PRIOR FILING DATE: 2001-01-12
; PRIOR APPLICATION NUMBER: US 60/261,457
; PRIOR FILING DATE: 2001-01-12
; PRIOR APPLICATION NUMBER: US 60/261,226
; PRIOR FILING DATE: 2001-01-12
; PRIOR APPLICATION NUMBER: US 60/261,304
; PRIOR FILING DATE: 2001-01-12
; PRIOR APPLICATION NUMBER: US 60/261,459
; PRIOR FILING DATE: 2001-01-12
; PRIOR APPLICATION NUMBER: US 60/261,456
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 76
; SOFTWARE: PatentIn version 3.1

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; SEQ ID NO 2
; LENGTH: 737
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-466-162-2

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Query Match          100.0%; Score 48; DB 34; Length 737;
Best Local Similarity 100.0%; Pred. No. 9.2;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      1 HDAPIGYD 8
        |||||
Db      85 HDAPIGYD 92

```

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RESULT 37
US-10-756-149-4713
; Sequence 4713, Application US/10756149
; GENERAL INFORMATION:
; APPLICANT: Aziz, Nataasha
; APPLICANT: Zlotnick, Albert
; TITLE OF INVENTION: NOVEL METHODS OF DIAGNOSIS OF METASTATIC CANCER, COMPOSITIONS AND
; TITLE OF INVENTION: METHODS OF SCREENING FOR MODULATORS OF METASTATIC CANCER
; FILE REFERENCE: file
; CURRENT APPLICATION NUMBER: US/10/756,149
; CURRENT FILING DATE: 2004-01-12
; NUMBER OF SEQ ID NOS: 5818
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4713
; LENGTH: 737
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-756-149-4713

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Query Match          100.0%; Score 48; DB 37; Length 737;
Best Local Similarity 100.0%; Pred. No. 9.2;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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```

QY      1 HDAPIGYD 8
        |||||
Db      85 HDAPIGYD 92

```

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RESULT 38
US-10-932-349-1540
; Sequence 1540, Application US/10932349
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele
; TITLE OF INVENTION: POLYMORPHISMS IN NUCLEIC ACID MOLECULES
; TITLE OF INVENTION: ENCODING HUMAN KINASE PROTEINS, METHODS OF DETECTION AND
; FILE REFERENCE: C0001483
; CURRENT APPLICATION NUMBER: US/10/932,349
; CURRENT FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 123188
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1540
; LENGTH: 737
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-932-349-1540

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Query Match          100.0%; Score 48; DB 39; Length 737;
Best Local Similarity 100.0%; Pred. No. 9.2;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      1 HDAPIGYD 8
        |||||
Db      85 HDAPIGYD 92

```

```

RESULT 39
US-11-152-366-28

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```

; Sequence 28, Application US/11152366
; GENERAL INFORMATION:
; APPLICANT: Brys, Reginald
; APPLICANT: Vandeghinste, Nick
; APPLICANT: Tomme, Peter H. M.
; TITLE OF INVENTION: Methods For Identification, And Compounds Useful For The
; TITLE OF INVENTION: Treatment Of Degenerative & Inflammatory Diseases
; FILE REFERENCE: P27,880-A USA
; CURRENT APPLICATION NUMBER: US/11/152,366
; CURRENT FILING DATE: 2005-06-14
; PRIOR APPLICATION NUMBER: 60/579,307
; PRIOR FILING DATE: 2004-06-14
; NUMBER OF SEQ ID NOS: 295
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 28
; LENGTH: 737
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-152-366-28

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```

Query Match          100.0%; Score 48; DB 41; Length 737;
Best Local Similarity 100.0%; Pred. No. 9.2;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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```

QY      1 HDAPIGYD 8
        |||||
Db      85 HDAPIGYD 92

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RESULT 40
US-60-452-680-12722
; Sequence 12722, Application US/60452680
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele
; APPLICANT: GROPE, Andrew
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: ALZHEIMER'S DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: C0001450
; CURRENT APPLICATION NUMBER: US/60/452,680
; CURRENT FILING DATE: 2003-03-07
; NUMBER OF SEQ ID NOS: 116213
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12722
; LENGTH: 737
; TYPE: PRT
; ORGANISM: Homo sapiens
US-60-452-680-12722

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```

Query Match          100.0%; Score 48; DB 48; Length 737;
Best Local Similarity 100.0%; Pred. No. 9.2;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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```

QY      1 HDAPIGYD 8
        |||||
Db      85 HDAPIGYD 92

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Search completed: December 3, 2005, 23:38:56
Job time : 568 secs

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Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 3, 2005, 23:24:54 : Search time 6 Seconds
(without alignments)
7.450 Million cell updates/sec

Title: US-10-807-553-2
Perfect score: 48
Sequence: 1 HDAPICVD 8

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 41035 seqs, 5587842 residues

Total number of hits satisfying chosen parameters: 41035

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database :

Pending Patents AA New:*
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3: /cgn2_6/ptodata/1/paa/US07_NEW_COMB.pep:*
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8: /cgn2_6/ptodata/1/paa/US60_NEW_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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1	48	100.0	8	7	US-11-271-285-1
2	44	91.7	8	7	US-11-271-285-3
3	44	91.7	8	7	US-11-271-285-9
4	43	89.6	8	7	US-11-271-285-4
5	42	87.5	8	7	US-11-271-285-5
6	40	83.3	8	7	US-11-271-285-8
7	40	83.3	8	7	US-11-271-285-10
8	36	75.0	8	7	US-11-271-285-2
9	36	75.0	8	7	US-11-271-285-13
10	35	72.9	8	7	US-11-271-285-6
11	35	72.9	8	7	US-11-271-285-7
12	31	64.6	8	7	US-11-271-285-12
13	29	60.4	8	1	PCT-US05-41373-24
14	29	60.4	261	7	US-11-274-683-24
15	29	60.4	515	8	US-60-732-162-964
16	29	60.4	877	6	US-10-244-081A-33
17	29	60.4	900	6	US-10-244-081A-20
18	28	58.3	136	7	US-11-218-976-19
19	28	58.3	388	7	US-11-218-976-21
20	28	58.3	578	8	US-60-732-162-404
21	28	58.3	683	6	US-10-380-533B-139
22	28	58.3	844	8	US-60-732-162-402
23	28	58.3	899	8	US-60-732-162-408
24	28	58.3	961	8	US-60-732-162-406
25	28	58.3	1199	7	US-11-271-139-2

26	28	58.3	1310	7	US-11-155-906-135	Sequence 135, App
27	28	58.3	1310	7	US-11-154-298-135	Sequence 135, App
28	28	58.3	1337	7	US-11-155-906-134	Sequence 134, App
29	28	58.3	1337	7	US-11-154-298-134	Sequence 134, App
30	28	58.3	1340	7	US-11-155-906-138	Sequence 138, App
31	28	58.3	1340	7	US-11-154-298-138	Sequence 138, App
32	28	58.3	1347	7	US-11-155-906-133	Sequence 133, App
33	28	58.3	1347	7	US-11-154-298-133	Sequence 133, App
34	27	56.2	5	7	US-11-271-285-14	Sequence 14, App
35	27	56.2	33	7	US-11-264-096-783	Sequence 73, App
36	26	54.2	13	7	US-11-152-974A-349	Sequence 349, App
37	26	54.2	13	7	US-11-153-143A-349	Sequence 349, App
38	26	54.2	30	6	US-10-868-184C-3480	Sequence 3480, App
39	26	54.2	148	6	US-10-206-921A-360	Sequence 360, App
40	26	54.2	163	6	US-10-267-849A-10	Sequence 10, App
41	26	54.2	243	7	US-11-265-762-68	Sequence 68, App
42	26	54.2	243	7	US-60-732-162-1654	Sequence 1654, App
43	26	54.2	290	8	US-60-731-733-2	Sequence 2, App
44	26	54.2	290	7	US-11-266-444-3231	Sequence 3231, App
45	26	54.2	290	8	US-60-735-988-3231	Sequence 3231, App
46	26	54.2	309	7	US-11-266-444-3230	Sequence 3230, App
47	26	54.2	309	8	US-60-735-988-3230	Sequence 3230, App
48	26	54.2	455	7	US-11-264-096-1401	Sequence 1401, App
49	26	54.2	481	1	PCT-US05-40306-36	Sequence 36, App
50	26	54.2	481	1	PCT-US05-40255-36	Sequence 36, App
51	26	54.2	481	1	PCT-US05-40256-41	Sequence 41, App
52	26	54.2	481	7	US-11-264-737-41	Sequence 41, App
53	26	54.2	481	7	US-11-265-761-36	Sequence 36, App
54	26	54.2	481	7	US-11-264-784-36	Sequence 36, App
55	26	54.2	678	7	US-11-202-507A-11	Sequence 11, App
56	26	54.2	679	7	US-11-202-507A-5	Sequence 5, App
57	26	54.2	720	6	US-10-206-917A-170	Sequence 170, App
58	26	54.2	1041	7	US-11-283-526-3	Sequence 3, App
59	26	54.2	1574	7	US-11-268-554-114	Sequence 114, App
60	26	54.2	1769	7	US-11-268-554-113	Sequence 113, App
61	26	54.2	2044	7	US-11-268-554-112	Sequence 112, App
62	26	54.2	2048	7	US-11-268-554-117	Sequence 117, App
63	26	54.2	2057	7	US-11-268-554-115	Sequence 115, App
64	26	54.2	2061	7	US-11-268-554-116	Sequence 116, App
65	26	54.2	3385	1	PCT-US05-41273-20	Sequence 20, App
66	26	54.2	3385	7	US-11-274-683-20	Sequence 20, App
67	25	52.1	20	7	US-11-266-444-2900	Sequence 2900, App
68	25	52.1	20	8	US-60-735-988-2900	Sequence 2900, App
69	25	52.1	43	6	US-10-253-471C-1490	Sequence 1490, App
70	25	52.1	55	6	US-10-469-469-193	Sequence 193, App
71	25	52.1	92	6	US-10-868-184C-4210	Sequence 4210, App
72	25	52.1	139	7	US-11-267-310-2	Sequence 2, App
73	25	52.1	139	7	US-11-267-191-2	Sequence 2, App
74	25	52.1	166	6	US-10-868-184C-3174	Sequence 3174, App
75	25	52.1	252	7	US-11-266-444-1416	Sequence 1416, App
76	25	52.1	252	8	US-60-735-988-1416	Sequence 1416, App
77	25	52.1	300	6	US-10-206-921A-18	Sequence 18, App
78	25	52.1	331	7	US-11-264-096-1257	Sequence 1257, App
79	25	52.1	331	7	US-11-197-712-243	Sequence 243, App
80	25	52.1	354	6	US-10-142-638A-70	Sequence 70, App
81	25	52.1	371	7	US-11-274-547-2	Sequence 2, App
82	25	52.1	377	7	US-11-267-310-55	Sequence 55, App
83	25	52.1	377	7	US-11-267-191-55	Sequence 55, App
84	25	52.1	383	7	US-11-267-310-57	Sequence 57, App
85	25	52.1	383	7	US-11-267-191-57	Sequence 57, App
86	25	52.1	391	6	US-10-556-478-2	Sequence 2, App
87	25	52.1	406	8	US-60-732-162-852	Sequence 852, App
88	25	52.1	420	6	US-60-732-162-852	Sequence 852, App
89	25	52.1	432	6	US-10-206-921A-330	Sequence 330, App
90	25	52.1	435	7	US-11-268-554-221	Sequence 221, App
91	25	52.1	437	7	US-11-268-554-220	Sequence 220, App
92	25	52.1	443	6	US-10-997-436-7	Sequence 7, App
93	25	52.1	461	6	US-10-556-478-3	Sequence 3, App
94	25	52.1	471	1	PCT-US05-40305-30	Sequence 30, App
95	25	52.1	471	1	PCT-US05-40256-35	Sequence 35, App
96	25	52.1	471	1	PCT-US05-40256-35	Sequence 35, App
97	25	52.1	471	7	US-11-264-737-35	Sequence 35, App
98	25	52.1	471	7	US-11-265-761-30	Sequence 30, App

99 25 52.1 471 7 US-11-264-784-30 Sequence 30, Appl
100 25 52.1 503 8 US-60-732-162-850 Sequence 850, App

ALIGNMENTS

RESULT 1
US-11-271-285-1
; Sequence 1, Application US/11271285
; GENERAL INFORMATION:
; APPLICANT: Mochly-Rosen, Darla
; APPLICANT: Tanaka, Masashi
; APPLICANT: Robbins, Robert C.
; TITLE OF INVENTION: Methods and Compositions for Reducing Injury to a Transplanted
; FILE REFERENCE: 58600-8218.US00
; CURRENT APPLICATION NUMBER: US/11/271,285
; CURRENT FILING DATE: 2005-11-10
; PRIOR APPLICATION NUMBER: US 60/626,564
; PRIOR FILING DATE: 2004-11-10
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-11-271-285-1

Query Match 100.0%; Score 48; DB 7; Length 8;
Best Local Similarity 100.0%; Pred. No. 3.3e+04;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HDAPIGYD 8
Db 1 HDAPIGYD 8

RESULT 2
US-11-271-285-3
; Sequence 3, Application US/11271285
; GENERAL INFORMATION:
; APPLICANT: Mochly-Rosen, Darla
; APPLICANT: Tanaka, Masashi
; APPLICANT: Robbins, Robert C.
; TITLE OF INVENTION: Methods and Compositions for Reducing Injury to a Transplanted
; FILE REFERENCE: 58600-8218.US00
; CURRENT APPLICATION NUMBER: US/11/271,285
; CURRENT FILING DATE: 2005-11-10
; PRIOR APPLICATION NUMBER: US 60/626,564
; PRIOR FILING DATE: 2004-11-10
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 3
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Peptide
US-11-271-285-3

Query Match 91.7%; Score 44; DB 7; Length 8;
Best Local Similarity 87.5%; Pred. No. 3.3e+04;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HDAPIGYD 8
Db 1 HDAPIGYD 8

RESULT 3
US-11-271-285-9

; Sequence 9, Application US/11271285
; GENERAL INFORMATION:
; APPLICANT: Mochly-Rosen, Darla
; APPLICANT: Tanaka, Masashi
; APPLICANT: Robbins, Robert C.
; TITLE OF INVENTION: Methods and Compositions for Reducing Injury to a Transplanted
; FILE REFERENCE: 58600-8218.US00
; CURRENT APPLICATION NUMBER: US/11/271,285
; CURRENT FILING DATE: 2005-11-10
; PRIOR APPLICATION NUMBER: US 60/626,564
; PRIOR FILING DATE: 2004-11-10
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 9
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Peptide
US-11-271-285-9

Query Match 91.7%; Score 44; DB 7; Length 8;
Best Local Similarity 87.5%; Pred. No. 3.3e+04;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 HDAPIGYD 8
Db 1 HDAPIGYD 8

RESULT 4
US-11-271-285-4
; Sequence 4, Application US/11271285
; GENERAL INFORMATION:
; APPLICANT: Mochly-Rosen, Darla
; APPLICANT: Tanaka, Masashi
; APPLICANT: Robbins, Robert C.
; TITLE OF INVENTION: Methods and Compositions for Reducing Injury to a Transplanted
; FILE REFERENCE: 58600-8218.US00
; CURRENT APPLICATION NUMBER: US/11/271,285
; CURRENT FILING DATE: 2005-11-10
; PRIOR APPLICATION NUMBER: US 60/626,564
; PRIOR FILING DATE: 2004-11-10
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 4
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Peptide
US-11-271-285-4

Query Match 89.6%; Score 43; DB 7; Length 8;
Best Local Similarity 75.0%; Pred. No. 3.3e+04;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HDAPIGYD 8
Db 1 HDAPIGYD 8

RESULT 5
US-11-271-285-5
; Sequence 5, Application US/11271285
; GENERAL INFORMATION:
; APPLICANT: Mochly-Rosen, Darla
; APPLICANT: Tanaka, Masashi
; APPLICANT: Robbins, Robert C.
; TITLE OF INVENTION: Methods and Compositions for Reducing Injury to a Transplanted
; FEATURE:
; OTHER INFORMATION: Synthetic Peptide
US-11-271-285-5

FILE REFERENCE: 58600-8218.US00
CURRENT APPLICATION NUMBER: US/11/271,285
CURRENT FILING DATE: 2005-11-10
PRIOR APPLICATION NUMBER: US 60/626,564
PRIOR FILING DATE: 2004-11-10
NUMBER OF SEQ ID NOS: 59
SOFTWARE: PatentIn version 3.3
SEQ ID NO 5
LENGTH: 8
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic Peptide
US-11-271-285-5

Query Match 87.5%; Score 42; DB 7; Length 8;
Best Local Similarity 75.0%; Pred. No. 3.3e+04;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 HDAPIGYD 8
|||:|
Db 1 HDAPLGYE 8

RESULT 6
US-11-271-285-8
Sequence 8, Application US/11271285
GENERAL INFORMATION:
APPLICANT: Mochly-Rosen, Daria
APPLICANT: Tanaka, Masashi
APPLICANT: Robbins, Robert C.
TITLE OF INVENTION: Methods and Compositions for Reducing Injury to a Transplanted
FILE REFERENCE: 58600-8218.US00
CURRENT APPLICATION NUMBER: US/11/271,285
CURRENT FILING DATE: 2005-11-10
PRIOR APPLICATION NUMBER: US 60/626,564
PRIOR FILING DATE: 2004-11-10
NUMBER OF SEQ ID NOS: 59
SOFTWARE: PatentIn version 3.3
SEQ ID NO 8
LENGTH: 8
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic Peptide
US-11-271-285-8

Query Match 83.3%; Score 40; DB 7; Length 8;
Best Local Similarity 100.0%; Pred. No. 3.3e+04;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DAPIGYD 8
|||||
Db 2 DAPIGYD 8

RESULT 7
US-11-271-285-10
Sequence 10, Application US/11271285
GENERAL INFORMATION:
APPLICANT: Mochly-Rosen, Daria
APPLICANT: Tanaka, Masashi
APPLICANT: Robbins, Robert C.
TITLE OF INVENTION: Methods and Compositions for Reducing Injury to a Transplanted
FILE REFERENCE: 58600-8218.US00
CURRENT APPLICATION NUMBER: US/11/271,285
CURRENT FILING DATE: 2005-11-10
PRIOR APPLICATION NUMBER: US 60/626,564
PRIOR FILING DATE: 2004-11-10
NUMBER OF SEQ ID NOS: 59
SOFTWARE: PatentIn version 3.3

SEQ ID NO 10
LENGTH: 8
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic Peptide
US-11-271-285-10

Query Match 83.3%; Score 40; DB 7; Length 8;
Best Local Similarity 87.5%; Pred. No. 3.3e+04;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 HDAPIGYD 8
|||||
Db 1 HDAPLGYD 8

RESULT 8
US-11-271-285-2
Sequence 2, Application US/11271285
GENERAL INFORMATION:
APPLICANT: Mochly-Rosen, Daria
APPLICANT: Tanaka, Masashi
APPLICANT: Robbins, Robert C.
TITLE OF INVENTION: Methods and Compositions for Reducing Injury to a Transplanted
FILE REFERENCE: 58600-8218.US00
CURRENT APPLICATION NUMBER: US/11/271,285
CURRENT FILING DATE: 2005-11-10
PRIOR APPLICATION NUMBER: US 60/626,564
PRIOR FILING DATE: 2004-11-10
NUMBER OF SEQ ID NOS: 59
SOFTWARE: PatentIn version 3.3
SEQ ID NO 2
LENGTH: 8
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic Peptide
US-11-271-285-2

Query Match 75.0%; Score 36; DB 7; Length 8;
Best Local Similarity 75.0%; Pred. No. 3.3e+04;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 HDAPIGYD 8
|||:|
Db 1 HDAPLGYD 8

RESULT 9
US-11-271-285-13
Sequence 13, Application US/11271285
GENERAL INFORMATION:
APPLICANT: Mochly-Rosen, Daria
APPLICANT: Tanaka, Masashi
APPLICANT: Robbins, Robert C.
TITLE OF INVENTION: Methods and Compositions for Reducing Injury to a Transplanted
FILE REFERENCE: 58600-8218.US00
CURRENT APPLICATION NUMBER: US/11/271,285
CURRENT FILING DATE: 2005-11-10
PRIOR APPLICATION NUMBER: US 60/626,564
PRIOR FILING DATE: 2004-11-10
NUMBER OF SEQ ID NOS: 59
SOFTWARE: PatentIn version 3.3
SEQ ID NO 13
LENGTH: 8
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic Peptide
US-11-271-285-13

Query Match 75.0%; Score 36; DB 7; Length 8;
Best Local Similarity 75.0%; Pred. No. 3.3e+04;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 HDAPIG 8
Db 1 HDGDI GVD 8

RESULT 10
US-11-271-285-6
; Sequence 6, Application US/11271285
; GENERAL INFORMATION:
; APPLICANT: Mochly-Rosen, Daria
; APPLICANT: Tanaka, Masashi
; APPLICANT: Robbins, Robert C.
; TITLE OF INVENTION: Methods and Compositions for Reducing Injury to a Transplanted
; FILE REFERENCE: 58600-8218.US00
; CURRENT APPLICATION NUMBER: US/11/271,285
; CURRENT FILING DATE: 2005-11-10
; PRIOR APPLICATION NUMBER: US 60/626,564
; PRIOR FILING DATE: 2004-11-10
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO: 6
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Peptide
US-11-271-285-6

Query Match 72.9%; Score 35; DB 7; Length 8;
Best Local Similarity 100.0%; Pred. No. 3.3e+04;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HDAPIG 6
Db 1 HDAPIG 6

RESULT 11
US-11-271-285-7
; Sequence 7, Application US/11271285
; GENERAL INFORMATION:
; APPLICANT: Mochly-Rosen, Daria
; APPLICANT: Tanaka, Masashi
; APPLICANT: Robbins, Robert C.
; TITLE OF INVENTION: Methods and Compositions for Reducing Injury to a Transplanted
; FILE REFERENCE: 58600-8218.US00
; CURRENT APPLICATION NUMBER: US/11/271,285
; CURRENT FILING DATE: 2005-11-10
; PRIOR APPLICATION NUMBER: US 60/626,564
; PRIOR FILING DATE: 2004-11-10
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO: 7
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Peptide
US-11-271-285-7

Query Match 72.9%; Score 35; DB 7; Length 8;
Best Local Similarity 100.0%; Pred. No. 3.3e+04;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HDAPIG 6
Db 1 HDAPIG 6

Db 1 HDAPIG 6

RESULT 12
US-11-271-285-12
; Sequence 12, Application US/11271285
; GENERAL INFORMATION:
; APPLICANT: Mochly-Rosen, Daria
; APPLICANT: Tanaka, Masashi
; APPLICANT: Robbins, Robert C.
; TITLE OF INVENTION: Methods and Compositions for Reducing Injury to a Transplanted
; FILE REFERENCE: 58600-8218.US00
; CURRENT APPLICATION NUMBER: US/11/271,285
; CURRENT FILING DATE: 2005-11-10
; PRIOR APPLICATION NUMBER: US 60/626,564
; PRIOR FILING DATE: 2004-11-10
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO: 12
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Peptide
US-11-271-285-12

Query Match 64.6%; Score 31; DB 7; Length 8;
Best Local Similarity 83.3%; Pred. No. 3.3e+04;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HDAPIG 6
Db 1 HDAPIG 6

RESULT 13
PCT-US05-41273-24
; Sequence 24, Application PC/TUS0541273
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Hailil, Bradley A
; TITLE OF INVENTION: Elatophyllin biosynthetic gene cluster
; FILE REFERENCE: 1855/257
; CURRENT APPLICATION NUMBER: PCT/US05/41273
; CURRENT FILING DATE: 2005-11-23
; PRIOR APPLICATION NUMBER: US 60/627,752
; PRIOR FILING DATE: 2004-11-12
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO: 24
; LENGTH: 261
; TYPE: PRT
; ORGANISM: Streptomyces sp. NRRL 30748
PCT-US05-41273-24

Query Match 60.4%; Score 29; DB 1; Length 261;
Best Local Similarity 100.0%; Pred. No. 36;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HDAPIG 5
Db 64 HDAPIG 68

RESULT 14
US-11-274-683-24
; Sequence 24, Application US/11274683
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Hailil, Bradley A
; TITLE OF INVENTION: Elatophyllin biosynthetic gene cluster
; FILE REFERENCE: 1855/256

; CURRENT APPLICATION NUMBER: US/11/274,683
; CURRENT FILING DATE: 2005-11-14
; PRIOR APPLICATION NUMBER: US 60/627,752
; PRIOR FILING DATE: 2004-11-12
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 24
; LENGTH: 261
; TYPE: PRT
; ORGANISM: Streptomyces sp. NRRL 30748
US-11-274-683-24

Query Match 60.4%; Score 29; DB 7; Length 261;
Best Local Similarity 100.0%; Pred. No. 36;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 HDAPI 5
Db 64 HDAPI 68

RESULT 15
US-60-732-162-964
; Sequence 964, Application US/60732162
; GENERAL INFORMATION:
; APPLICANT: Belouchi, Abdelmajid
; APPLICANT: Raelson, John V
; APPLICANT: Bradley, Walter E
; APPLICANT: Paquin, Bruno
; APPLICANT: Fournier, Helene
; APPLICANT: Nguyen-Huu, Quynh
; APPLICANT: Croteau, Pascal
; APPLICANT: Allard, Rene
; APPLICANT: Debrus, Sophie
; APPLICANT: Berdewegh, Paul V
; APPLICANT: Little, Randall D
; APPLICANT: Keith, Tim
; APPLICANT: Segal, Jonathan
; TITLE OF INVENTION: Genemap of the Human Genes Associated with Asthma Disease
; FILE REFERENCE: 059908-5010-PR
; CURRENT APPLICATION NUMBER: US/60/732,162
; CURRENT FILING DATE: 2005-11-02
; NUMBER OF SEQ ID NOS: 4417
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 964
; LENGTH: 515
; TYPE: PRT
; ORGANISM: Homosapiens
US-60-732-162-964

Query Match 60.4%; Score 29; DB 8; Length 515;
Best Local Similarity 83.3%; Pred. No. 75;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 DAPIGY 7
Db 129 DAPIGY 134

RESULT 16
US-10-244-081A-33
; Sequence 33, Application US/10244081A
; GENERAL INFORMATION:
; APPLICANT: Lee, Jun
; APPLICANT: Gerard, Gary
; APPLICANT: Shandilya, Harini
; APPLICANT: Griffiths, Katherine Rachel
; APPLICANT: Gibbs, Moreland David
; APPLICANT: Leonard, Peter
; APPLICANT: Bergquist, Peter Leonard
; APPLICANT: Potter, Jason
; TITLE OF INVENTION: DNA Polymerases and Mutants Thereof
; FILE REFERENCE: 0942.536001

; CURRENT APPLICATION NUMBER: US/10/244,081A
; CURRENT FILING DATE: 2002-09-16
; PRIOR APPLICATION NUMBER: US 60/318,903
; PRIOR FILING DATE: 2001-09-14
; NUMBER OF SEQ ID NOS: 3641
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 33
; LENGTH: 877
; TYPE: PRT
; ORGANISM: Bacillus caldolenax
US-10-244-081A-33

Query Match 60.4%; Score 29; DB 6; Length 877;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 HDAPI 5
Db 328 HDAPI 332

RESULT 17
US-10-244-081A-20
; Sequence 20, Application US/10244081A
; GENERAL INFORMATION:
; APPLICANT: Lee, Jun
; APPLICANT: Gerard, Gary
; APPLICANT: Shandilya, Harini
; APPLICANT: Griffiths, Katherine Rachel
; APPLICANT: Gibbs, Moreland David
; APPLICANT: Leonard, Peter
; APPLICANT: Bergquist, Peter Leonard
; APPLICANT: Potter, Jason
; TITLE OF INVENTION: DNA Polymerases and Mutants Thereof
; FILE REFERENCE: 0942.536001
; CURRENT APPLICATION NUMBER: US/10/244,081A
; CURRENT FILING DATE: 2002-09-16
; PRIOR APPLICATION NUMBER: US 60/318,903
; PRIOR FILING DATE: 2001-09-14
; NUMBER OF SEQ ID NOS: 3641
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 20
; LENGTH: 900
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Bacillus caldolyticus EAI DNA polymerase
US-10-244-081A-20

Query Match 60.4%; Score 29; DB 6; Length 900;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 HDAPI 5
Db 352 HDAPI 356

RESULT 18
US-11-218-976-19
; Sequence 19, Application US/11218976
; GENERAL INFORMATION:
; APPLICANT: Bertozzi, Carolyn
; APPLICANT: Williams, Spencer J.
; APPLICANT: Mougous, Joseph
; TITLE OF INVENTION: Mycobacterial Sulfation Pathway Proteins
; FILE REFERENCE: BERK-012DIY2
; CURRENT APPLICATION NUMBER: US/11/218,976
; CURRENT FILING DATE: 2005-09-01
; PRIOR APPLICATION NUMBER: 10/286,606
; PRIOR FILING DATE: 2002-10-31
; PRIOR APPLICATION NUMBER: 10/891,383

```

/ PRIOR FILING DATE: 2002-10-31
/ PRIOR APPLICATION NUMBER: 60/285,394
/ PRIOR FILING DATE: 2001-04-20
/ PRIOR APPLICATION NUMBER: 60/345,953
/ PRIOR FILING DATE: 2001-10-26
/ PRIOR APPLICATION NUMBER: 10/126,279
/ PRIOR FILING DATE: 2002-04-19
/ NUMBER OF SEQ ID NOS: 60
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 19
/ LENGTH: 136
/ TYPE: PRT
/ ORGANISM: Mycobacterium bovis
US-11-218-976-19

```

```

Query Match      58.3%; Score 28; DB 7; Length 136;
Best Local Similarity 50.0%; Pred. No. 29;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

```

```

Qy      1 HDAPGYD 8
Db      28 HTGPGYE 35

```

```

RESULT 19
US-11-218-976-21
/ Sequence 21, Application US/11218976
/ GENERAL INFORMATION:
/ APPLICANT: Bertozzi, Carolyn
/ APPLICANT: Williams, Spencer J.
/ APPLICANT: Mougous, Joseph
/ TITLE OF INVENTION: Mycobacterial Sulfation Pathway Proteins
/ FILE REFERENCE: BERK-012DIV2
/ CURRENT APPLICATION NUMBER: US/11/218,976
/ CURRENT FILING DATE: 2005-09-01
/ PRIOR APPLICATION NUMBER: 10/286,606
/ PRIOR FILING DATE: 2002-10-31
/ PRIOR APPLICATION NUMBER: 10/891,383
/ PRIOR FILING DATE: 2002-10-31
/ PRIOR APPLICATION NUMBER: 60/285,394
/ PRIOR FILING DATE: 2001-04-20
/ PRIOR APPLICATION NUMBER: 60/345,953
/ PRIOR FILING DATE: 2001-10-26
/ PRIOR APPLICATION NUMBER: 10/126,279
/ PRIOR FILING DATE: 2002-04-19
/ NUMBER OF SEQ ID NOS: 60
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 21
/ LENGTH: 388
/ TYPE: PRT
/ ORGANISM: Mycobacterium tuberculosis
US-11-218-976-21

```

```

Query Match      58.3%; Score 28; DB 7; Length 388;
Best Local Similarity 50.0%; Pred. No. 88;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

```

```

Qy      1 HDAPGYD 8
Db      106 HTGPGYE 113

```

```

RESULT 20
US-60-732-162-404
/ Sequence 404, Application US/60732162
/ GENERAL INFORMATION:
/ APPLICANT: Belouchi, Abdelmajid
/ APPLICANT: Raelson, John V
/ APPLICANT: Bradley, Walter E
/ APPLICANT: Paquin, Bruno
/ APPLICANT: Fournier, Helene
/ APPLICANT: Nguyen-Huu, Quynh

```

```

/ APPLICANT: Croteau, Pascal
/ APPLICANT: Allard, Rene
/ APPLICANT: Debrus, Sophie
/ APPLICANT: Berdewesh, Paul V
/ APPLICANT: Little, Randall D
/ APPLICANT: Keith, Tim
/ APPLICANT: Segal, Jonathan
/ TITLE OF INVENTION: Genesap of the Human Genes Associated With Asthma Disease
/ FILE REFERENCE: 059908-5010-PR
/ CURRENT APPLICATION NUMBER: US/60/732,162
/ CURRENT FILING DATE: 2005-11-02
/ NUMBER OF SEQ ID NOS: 4417
/ SOFTWARE: Patentin version 3.3
/ SEQ ID NO 404
/ LENGTH: 578
/ TYPE: PRT
/ ORGANISM: Homosapiens
US-60-732-162-404

```

```

Query Match      58.3%; Score 28; DB 8; Length 578;
Best Local Similarity 57.1%; Pred. No. 1,3e+02;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

```

```

Qy      2 DAPGYD 8
Db      466 EAPLAYD 472

```

```

RESULT 21
US-10-380-533B-139
/ Sequence 139, Application US/10380533B
/ GENERAL INFORMATION:
/ APPLICANT: University College Cardiff Consultants Ltd
/ TITLE OF INVENTION: Transglutaminase Gene Products
/ FILE REFERENCE: P504074PCT
/ CURRENT APPLICATION NUMBER: US/10/380,533B
/ CURRENT FILING DATE: 2003-09-30
/ PRIOR APPLICATION NUMBER: GB0111995.7
/ PRIOR FILING DATE: 2001-05-16
/ PRIOR APPLICATION NUMBER: GB0022768.6
/ PRIOR FILING DATE: 2000-09-15
/ NUMBER OF SEQ ID NOS: 144
/ SOFTWARE: Patentin version 3.1
/ SEQ ID NO 139
/ LENGTH: 683
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-380-533B-139

```

```

Query Match      58.3%; Score 28; DB 6; Length 683;
Best Local Similarity 71.4%; Pred. No. 1.6e+02;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```

```

Qy      2 DAPGYD 8
Db      337 DLPKGYD 343

```

```

RESULT 22
US-60-732-162-402
/ Sequence 402, Application US/60732162
/ GENERAL INFORMATION:
/ APPLICANT: Belouchi, Abdelmajid
/ APPLICANT: Raelson, John V
/ APPLICANT: Bradley, Walter E
/ APPLICANT: Paquin, Bruno
/ APPLICANT: Fournier, Helene
/ APPLICANT: Nguyen-Huu, Quynh
/ APPLICANT: Croteau, Pascal
/ APPLICANT: Allard, Rene
/ APPLICANT: Debrus, Sophie
/ APPLICANT: Berdewesh, Paul V
/ APPLICANT: Little, Randall D

```

```
; APPLICANT: Keith, Tim
; APPLICANT: Segal, Jonathan
; TITLE OF INVENTION: Genemap of the Human Genes Associated With Asthma Disease
; FILE REFERENCE: 059908-5010-PR
; CURRENT APPLICATION NUMBER: US/60/732,162
; CURRENT FILING DATE: 2005-11-02
; NUMBER OF SEQ ID NOS: 4417
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 402
; LENGTH: 844
; TYPE: PRT
; ORGANISM: Homosapiens
US-60-732-162-402
```

```
Query Match      58.3%; Score 28; DB 8; Length 844;
Best Local Similarity 57.1%; Pred. No. 2e+02;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      2 DAPIGYD 8
      :||: ||
Db      349 EAPLAYD 355
```

```
RESULT 23
US-60-732-162-408
; Sequence 408, Application US/60732162
; GENERAL INFORMATION:
; APPLICANT: Belouchi, Abdelmajid
; APPLICANT: Raelson, John V
; APPLICANT: Bradley, Walter E
; APPLICANT: Paquin, Bruno
; APPLICANT: Fournier, Helene
; APPLICANT: Nguyen-Huu, Quynh
; APPLICANT: Croteau, Pascal
; APPLICANT: Allard, Rene
; APPLICANT: Debrus, Sophie
; APPLICANT: Berdewegh, Paul V
; APPLICANT: Little, Randall D
; APPLICANT: Keith, Tim
; APPLICANT: Segal, Jonathan
; TITLE OF INVENTION: Genemap of the Human Genes Associated With Asthma Disease
; FILE REFERENCE: 059908-5010-PR
; CURRENT APPLICATION NUMBER: US/60/732,162
; CURRENT FILING DATE: 2005-11-02
; NUMBER OF SEQ ID NOS: 4417
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 408
; LENGTH: 899
; TYPE: PRT
; ORGANISM: Homosapiens
US-60-732-162-408
```

```
Query Match      58.3%; Score 28; DB 8; Length 899;
Best Local Similarity 57.1%; Pred. No. 2.2e+02;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      2 DAPIGYD 8
      :||: ||
Db      404 EAPLAYD 410
```

```
RESULT 24
US-60-732-162-406
; Sequence 406, Application US/60732162
; GENERAL INFORMATION:
; APPLICANT: Belouchi, Abdelmajid
; APPLICANT: Raelson, John V
; APPLICANT: Bradley, Walter E
; APPLICANT: Paquin, Bruno
; APPLICANT: Fournier, Helene
; APPLICANT: Nguyen-Huu, Quynh
; APPLICANT: Croteau, Pascal
; APPLICANT: Allard, Rene
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; APPLICANT: Debrus, Sophie
; APPLICANT: Berdewegh, Paul V
; APPLICANT: Little, Randall D
; APPLICANT: Keith, Tim
; APPLICANT: Segal, Jonathan
; TITLE OF INVENTION: Genemap of the Human Genes Associated With Asthma Disease
; FILE REFERENCE: 059908-5010-PR
; CURRENT APPLICATION NUMBER: US/60/732,162
; CURRENT FILING DATE: 2005-11-02
; NUMBER OF SEQ ID NOS: 4417
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 406
; LENGTH: 961
; TYPE: PRT
; ORGANISM: Homosapiens
US-60-732-162-406
```

```
Query Match      58.3%; Score 28; DB 8; Length 961;
Best Local Similarity 57.1%; Pred. No. 2.3e+02;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      2 DAPIGYD 8
      :||: ||
Db      466 EAPLAYD 472
```

```
RESULT 25
US-11-271-139-2
; Sequence 2, Application US/11271139
; GENERAL INFORMATION:
; APPLICANT: Allen, Keith D.
; TITLE OF INVENTION: METABOTROPIC GLUTAMATE RECEPTOR 1
; FILE REFERENCE: R-801
; CURRENT APPLICATION NUMBER: US/11/271,139
; CURRENT FILING DATE: 2005-11-10
; PRIOR APPLICATION NUMBER: US/10/179,408
; PRIOR FILING DATE: 2002-06-24
; PRIOR APPLICATION NUMBER: US 60/301,061
; PRIOR FILING DATE: 2001-06-26
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 1199
; TYPE: PRT
; ORGANISM: Mus musculus
US-11-271-139-2
```

```
Query Match      58.3%; Score 28; DB 7; Length 1199;
Best Local Similarity 66.7%; Pred. No. 2.9e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      3 APIGYD 8
      :||: ||
Db      755 APIGCYN 760
```

```
RESULT 26
US-11-155-906-135
; Sequence 135, Application US/11155906
; GENERAL INFORMATION:
; APPLICANT: Jakobovits, Aya
; APPLICANT: Chailita-Bld, Pia M.
; APPLICANT: Paris, Mary
; APPLICANT: Ge, Wangmao
; APPLICANT: Hubert, Rene S.
; APPLICANT: Morrison, Karen Jane Meyrick
; APPLICANT: Morrison, Robert Kendall
; APPLICANT: Raitano, Arthur B.
; TITLE OF INVENTION: METHODS OF INDUCING AN IMMUNE RESPONSE
; FILE REFERENCE: 51158-20040.02
; CURRENT APPLICATION NUMBER: US/11/155,906
; CURRENT FILING DATE: 2005-06-17
```

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; PRIOR APPLICATION NUMBER: US10/121,024
; PRIOR FILING DATE: 2002-04-10
; PRIOR APPLICATION NUMBER: US60/283,112
; PRIOR FILING DATE: 2001-04-10
; PRIOR APPLICATION NUMBER: US60/282,739
; PRIOR FILING DATE: 2001-04-10
; PRIOR APPLICATION NUMBER: US60/286,630
; PRIOR FILING DATE: 2001-04-25
; NUMBER OF SEQ ID NOS: 708
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 135
; LENGTH: 1310
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-155-906-135

Query Match          58.3% Score 28; DB 7; Length 1310;
Best Local Similarity 57.1% Pred. No. 3.2e+02;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      1 HDAPIGY 7
DB      1046 HGLPLGY 1052

RESULT 27
US-11-154-298-135
; Sequence 135, Application US/11154298
; GENERAL INFORMATION:
; APPLICANT: Jakobovits, Aya
; APPLICANT: Chailita-Bid, Pia M.
; APPLICANT: Ge, Mangmao
; APPLICANT: Hubert, Rene S.
; APPLICANT: Morrison, Karen Jane Meyrick
; APPLICANT: Raitano, Robert Kendall
; APPLICANT: Raitano, Arthur B.
; TITLE OF INVENTION: METHODS OF INDUCING AN IMMUNE RESPONSE
; FILE REFERENCE: 51158-20040.01
; CURRENT APPLICATION NUMBER: US/11/154,298
; CURRENT FILING DATE: 2005-06-15
; PRIOR APPLICATION NUMBER: US10/121,024
; PRIOR FILING DATE: 2002-04-10
; PRIOR APPLICATION NUMBER: US60/283,112
; PRIOR FILING DATE: 2001-04-10
; PRIOR APPLICATION NUMBER: US60/282,739
; PRIOR FILING DATE: 2001-04-10
; PRIOR APPLICATION NUMBER: US60/286,630
; PRIOR FILING DATE: 2001-04-25
; NUMBER OF SEQ ID NOS: 708
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 135
; LENGTH: 1310
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-154-298-135

Query Match          58.3% Score 28; DB 7; Length 1310;
Best Local Similarity 57.1% Pred. No. 3.2e+02;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      1 HDAPIGY 7
DB      1046 HGLPLGY 1052

RESULT 28
US-11-155-906-134
; Sequence 134, Application US/11155906
; GENERAL INFORMATION:
; APPLICANT: Jakobovits, Aya
; APPLICANT: Chailita-Bid, Pia M.
; APPLICANT: Farris, Mary
```

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; APPLICANT: Ge, Mangmao
; APPLICANT: Hubert, Rene S.
; APPLICANT: Morrison, Karen Jane Meyrick
; APPLICANT: Raitano, Robert Kendall
; APPLICANT: Raitano, Arthur B.
; TITLE OF INVENTION: METHODS OF INDUCING AN IMMUNE RESPONSE
; FILE REFERENCE: 51158-20040.02
; CURRENT APPLICATION NUMBER: US/11/155,906
; CURRENT FILING DATE: 2005-06-17
; PRIOR APPLICATION NUMBER: US10/121,024
; PRIOR FILING DATE: 2002-04-10
; PRIOR APPLICATION NUMBER: US60/283,112
; PRIOR FILING DATE: 2001-04-10
; PRIOR APPLICATION NUMBER: US60/282,739
; PRIOR FILING DATE: 2001-04-10
; PRIOR APPLICATION NUMBER: US60/286,630
; PRIOR FILING DATE: 2001-04-25
; NUMBER OF SEQ ID NOS: 708
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 134
; LENGTH: 1337
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-154-298-134

Query Match          58.3% Score 28; DB 7; Length 1337;
Best Local Similarity 57.1% Pred. No. 3.3e+02;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      1 HDAPIGY 7
DB      1073 HGLPLGY 1079

RESULT 29
US-11-154-298-134
; Sequence 134, Application US/11154298
; GENERAL INFORMATION:
; APPLICANT: Jakobovits, Aya
; APPLICANT: Chailita-Bid, Pia M.
; APPLICANT: Farris, Mary
; APPLICANT: Ge, Mangmao
; APPLICANT: Hubert, Rene S.
; APPLICANT: Morrison, Karen Jane Meyrick
; APPLICANT: Raitano, Robert Kendall
; APPLICANT: Raitano, Arthur B.
; TITLE OF INVENTION: METHODS OF INDUCING AN IMMUNE RESPONSE
; FILE REFERENCE: 51158-20040.01
; CURRENT APPLICATION NUMBER: US/11/154,298
; CURRENT FILING DATE: 2005-06-15
; PRIOR APPLICATION NUMBER: US10/121,024
; PRIOR FILING DATE: 2002-04-10
; PRIOR APPLICATION NUMBER: US60/283,112
; PRIOR FILING DATE: 2001-04-10
; PRIOR APPLICATION NUMBER: US60/282,739
; PRIOR FILING DATE: 2001-04-10
; PRIOR APPLICATION NUMBER: US60/286,630
; PRIOR FILING DATE: 2001-04-25
; NUMBER OF SEQ ID NOS: 708
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 134
; LENGTH: 1337
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-154-298-134

Query Match          58.3% Score 28; DB 7; Length 1337;
Best Local Similarity 57.1% Pred. No. 3.3e+02;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      1 HDAPIGY 7
DB      1073 HGLPLGY 1079
```

```
RESULT 30
US-11-155-906-138
; Sequence 138, Application US/11155906
; GENERAL INFORMATION:
; APPLICANT: Jakobovits, Aya
; APPLICANT: Chailita-Eld, Pia M.
; APPLICANT: Farris, Mary
; APPLICANT: Ge, Wangmao
; APPLICANT: Hubert, Rene S.
; APPLICANT: Morrison, Karen Jane Meyrick
; APPLICANT: Morrison, Robert Kendall
; APPLICANT: Raitano, Arthur B.
; TITLE OF INVENTION: METHODS OF INDUCING AN IMMUNE RESPONSE
; FILE REFERENCE: 51158-20040.02
; CURRENT APPLICATION NUMBER: US/11/155,906
; PRIOR FILING DATE: 2005-06-17
; PRIOR APPLICATION NUMBER: US10/121,024
; PRIOR FILING DATE: 2002-04-10
; PRIOR APPLICATION NUMBER: US60/283,112
; PRIOR FILING DATE: 2001-04-10
; PRIOR APPLICATION NUMBER: US60/282,739
; PRIOR FILING DATE: 2001-04-10
; PRIOR APPLICATION NUMBER: US60/286,630
; PRIOR FILING DATE: 2001-04-25
; NUMBER OF SEQ ID NOS: 708
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 138
; LENGTH: 1340
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-155-906-138

Query Match          58.3%; Score 28; DB 7; Length 1340;
Best Local Similarity 57.1%; Pred. NO. 3.3e+02;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      1 HDAPIGY 7
Db      1078 HGLPLGY 1084

RESULT 31
US-11-154-298-138
; Sequence 138, Application US/11154298
; GENERAL INFORMATION:
; APPLICANT: Jakobovits, Aya
; APPLICANT: Chailita-Eld, Pia M.
; APPLICANT: Farris, Mary
; APPLICANT: Ge, Wangmao
; APPLICANT: Hubert, Rene S.
; APPLICANT: Morrison, Karen Jane Meyrick
; APPLICANT: Morrison, Robert Kendall
; APPLICANT: Raitano, Arthur B.
; TITLE OF INVENTION: METHODS OF INDUCING AN IMMUNE RESPONSE
; FILE REFERENCE: 51158-20040.01
; CURRENT APPLICATION NUMBER: US/11/154,298
; PRIOR FILING DATE: 2005-06-15
; PRIOR APPLICATION NUMBER: US10/121,024
; PRIOR FILING DATE: 2002-04-10
; PRIOR APPLICATION NUMBER: US60/283,112
; PRIOR FILING DATE: 2001-04-10
; PRIOR APPLICATION NUMBER: US60/282,739
; PRIOR FILING DATE: 2001-04-10
; PRIOR APPLICATION NUMBER: US60/286,630
; PRIOR FILING DATE: 2001-04-25
; NUMBER OF SEQ ID NOS: 708
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 138
; LENGTH: 1340
; TYPE: PRT
; ORGANISM: Homo sapiens
```

```
US-11-154-298-138

Query Match          58.3%; Score 28; DB 7; Length 1340;
Best Local Similarity 57.1%; Pred. NO. 3.3e+02;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      1 HDAPIGY 7
Db      1078 HGLPLGY 1084

RESULT 32
US-11-155-906-133
; Sequence 133, Application US/11155906
; GENERAL INFORMATION:
; APPLICANT: Jakobovits, Aya
; APPLICANT: Chailita-Eld, Pia M.
; APPLICANT: Farris, Mary
; APPLICANT: Ge, Wangmao
; APPLICANT: Hubert, Rene S.
; APPLICANT: Morrison, Karen Jane Meyrick
; APPLICANT: Morrison, Robert Kendall
; APPLICANT: Raitano, Arthur B.
; TITLE OF INVENTION: METHODS OF INDUCING AN IMMUNE RESPONSE
; FILE REFERENCE: 51158-20040.02
; CURRENT APPLICATION NUMBER: US/11/155,906
; PRIOR FILING DATE: 2005-06-17
; PRIOR APPLICATION NUMBER: US10/121,024
; PRIOR FILING DATE: 2002-04-10
; PRIOR APPLICATION NUMBER: US60/283,112
; PRIOR FILING DATE: 2001-04-10
; PRIOR APPLICATION NUMBER: US60/282,739
; PRIOR FILING DATE: 2001-04-10
; PRIOR APPLICATION NUMBER: US60/286,630
; PRIOR FILING DATE: 2001-04-25
; NUMBER OF SEQ ID NOS: 708
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 133
; LENGTH: 1347
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-155-906-133

Query Match          58.3%; Score 28; DB 7; Length 1347;
Best Local Similarity 57.1%; Pred. NO. 3.3e+02;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      1 HDAPIGY 7
Db      1083 HGLPLGY 1089

RESULT 33
US-11-154-298-133
; Sequence 133, Application US/11154298
; GENERAL INFORMATION:
; APPLICANT: Jakobovits, Aya
; APPLICANT: Chailita-Eld, Pia M.
; APPLICANT: Farris, Mary
; APPLICANT: Ge, Wangmao
; APPLICANT: Hubert, Rene S.
; APPLICANT: Morrison, Karen Jane Meyrick
; APPLICANT: Morrison, Robert Kendall
; APPLICANT: Raitano, Arthur B.
; TITLE OF INVENTION: METHODS OF INDUCING AN IMMUNE RESPONSE
; FILE REFERENCE: 51158-20040.01
; CURRENT APPLICATION NUMBER: US/11/154,298
; PRIOR FILING DATE: 2005-06-15
; PRIOR APPLICATION NUMBER: US10/121,024
; PRIOR FILING DATE: 2002-04-10
; PRIOR APPLICATION NUMBER: US60/283,112
; PRIOR FILING DATE: 2001-04-10
; PRIOR APPLICATION NUMBER: US60/282,739
```

```
; PRIOR FILING DATE: 2001-04-10
; PRIOR APPLICATION NUMBER: US60/286,630
; PRIOR FILING DATE: 2001-04-25
; NUMBER OF SEQ ID NOS: 708
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 133
; LENGTH: 1347
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-154-298-133

Query Match
Best Local Similarity 58.3%; Score 28; DB 7; Length 1347;
Pred. No. 3.3e+02;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 HDAPIG 7
Db 1083 HGLPLGY 1089

RESULT 34
US-11-271-285-14
; Sequence 14, Application US/11271285
; GENERAL INFORMATION:
; APPLICANT: Mochly-Rosen, Daria
; APPLICANT: Tanaka, Masashi
; APPLICANT: Robbins, Robert C.
; TITLE OF INVENTION: Methods and Compositions for Reducing Injury to a Transplanted
; TITLE OF INVENTION: Organ
; FILE REFERENCE: 5860-8218.US00
; CURRENT APPLICATION NUMBER: US/11/271,285
; CURRENT FILING DATE: 2005-11-10
; PRIOR APPLICATION NUMBER: US 60/626,564
; PRIOR FILING DATE: 2004-11-10
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 14
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Peptide
US-11-271-285-14

Query Match
Best Local Similarity 56.2%; Score 27; DB 7; Length 5;
Pred. No. 3.3e+04;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 DAPIG 6
Db 1 DAPIG 5

RESULT 35
US-11-264-096-783
; Sequence 783, Application US/11264096
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Albumin Fusion Proteins
; FILE REFERENCE: PFS46D1
; CURRENT APPLICATION NUMBER: US/11/264,096
; CURRENT FILING DATE: 2005-11-02
; PRIOR APPLICATION NUMBER: 09/833,245
; PRIOR FILING DATE: 2001-04-12
; PRIOR APPLICATION NUMBER: 60/229,358
; PRIOR FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: 60/256,931
; PRIOR FILING DATE: 2000-12-21
; PRIOR APPLICATION NUMBER: 60/199,384
; PRIOR FILING DATE: 2000-04-25
; NUMBER OF SEQ ID NOS: 2267
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 783
```

```
; LENGTH: 33
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-264-096-783

Query Match
Best Local Similarity 56.2%; Score 27; DB 7; Length 33;
Pred. No. 10;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 HDAPIG 6
Db 21 HPAPVG 26

RESULT 36
US-11-152-974A-349
; Sequence 349, Application US/11152974A
; GENERAL INFORMATION:
; APPLICANT: Wayne F. Beyer, Jr.
; APPLICANT: Robin Hyde-Deruysscher
; APPLICANT: Paul T. Hamilton
; APPLICANT: Ray Edward Benson
; TITLE OF INVENTION: IFMbs to Promote the Specific Attachment of Target Analytes to the
; TITLE OF INVENTION: of Orthopedic Implants
; FILE REFERENCE: AFP006
; CURRENT APPLICATION NUMBER: US/11/152,974A
; CURRENT FILING DATE: 2005-06-15
; PRIOR APPLICATION NUMBER: 60/580,019
; PRIOR FILING DATE: 2004-06-16
; PRIOR APPLICATION NUMBER: 60/651,338
; PRIOR FILING DATE: 2005-02-09
; PRIOR APPLICATION NUMBER: 60/651,747
; PRIOR FILING DATE: 2005-02-10
; NUMBER OF SEQ ID NOS: 558
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 349
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Isolated from phage display libraries
US-11-152-974A-349

Query Match
Best Local Similarity 54.2%; Score 26; DB 7; Length 13;
Pred. No. 5.9;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 3 APGYD 8
Db 8 SPAGYD 13

RESULT 37
US-11-153-143A-349
; Sequence 349, Application US/11153143A
; GENERAL INFORMATION:
; APPLICANT: Paul T. Hamilton
; APPLICANT: Mark W. Grinstaff
; APPLICANT: Daniel J. Kenan
; APPLICANT: Dale J. Christensen
; TITLE OF INVENTION: Biofunctional Coatings
; FILE REFERENCE: AFP005
; CURRENT APPLICATION NUMBER: US/11/153,143A
; CURRENT FILING DATE: 2005-06-15
; PRIOR APPLICATION NUMBER: 60/580,019
; PRIOR FILING DATE: 2004-06-16
; PRIOR APPLICATION NUMBER: 60/651,338
; PRIOR FILING DATE: 2005-02-09
; PRIOR APPLICATION NUMBER: 60/651,747
; PRIOR FILING DATE: 2005-02-10
; NUMBER OF SEQ ID NOS: 558
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 349
```

```

; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: isolated from phage display libraries
US-11-153-143A-349

Query Match          54.2%; Score 26; DB 7; Length 13;
Best Local Similarity 66.7%; Pred. No. 5.9;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      3 APGYD 8
      :|:|:|
Db      8 SPAGYD 13

RESULT 38
US-10-868-184C-3480
; Sequence 3480, Application US/10868184C
; GENERAL INFORMATION:
; APPLICANT: Rosen, et. al
; TITLE OF INVENTION: Human Secreted Proteins
; FILE REFERENCE: P8805
; CURRENT APPLICATION NUMBER: US/10/868,184C
; CURRENT FILING DATE: 2004-06-16
; PRIOR APPLICATION NUMBER: 60/278,650
; PRIOR FILING DATE: 2001-03-27
; PRIOR APPLICATION NUMBER: 09/833,245
; PRIOR FILING DATE: 2001-04-12
; PRIOR APPLICATION NUMBER: PCT/US01/11988
; PRIOR FILING DATE: 2001-04-12
; PRIOR APPLICATION NUMBER: PCT/US00/06043
; PRIOR FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: PCT/US00/06012
; PRIOR FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: PCT/US00/06058
; PRIOR FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: PCT/US00/06044
; PRIOR FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: PCT/US00/06059
; PRIOR FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: PCT/US00/06042
; PRIOR FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: PCT/US00/06014
; PRIOR FILING DATE: 2000-03-09
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 13046
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3480
; LENGTH: 30
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-868-184C-3480

Query Match          54.2%; Score 26; DB 6; Length 30;
Best Local Similarity 57.1%; Pred. No. 14;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      1 HDAPGY 7
      :|:|:|
Db      20 HELPGY 26

RESULT 39
US-10-206-921A-360
; Sequence 360, Application US/10206921A
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
```

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; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zhenli
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: 39780-3430R1C515
; CURRENT APPLICATION NUMBER: US/10/206,921A
; CURRENT FILING DATE: 2002-07-26
; PRIOR APPLICATION NUMBER: US 10/052,586
; PRIOR FILING DATE: 2002-01-15
; PRIOR APPLICATION NUMBER: PCT/US01/06520
; PRIOR FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: US 60/232,887
; PRIOR FILING DATE: 2000-09-15
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 360
; LENGTH: 148
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-206-921A-360

Query Match          54.2%; Score 26; DB 6; Length 148;
Best Local Similarity 50.0%; Pred. No. 79;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY      1 HDAPGYD 8
      :|:|:|
Db      139 HGASVNYD 146

RESULT 40
US-10-267-849A-10
; Sequence 10, Application US/10267849A
; GENERAL INFORMATION:
; APPLICANT: Ji et al.
; TITLE OF INVENTION: Breast Specific Genes and Proteins
; FILE REFERENCE: P158C1
; CURRENT APPLICATION NUMBER: US/10/267,849A
; CURRENT FILING DATE: 2002-10-10
; PRIOR APPLICATION NUMBER: US 08/673,284
; PRIOR FILING DATE: 1996-06-28
; PRIOR APPLICATION NUMBER: US 60/000,602
; PRIOR FILING DATE: 1995-06-30
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
; LENGTH: 163
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (14)..(14)
; OTHER INFORMATION: The 'Xaa' at location 14 stands for Lys, Asn, Arg, Ser, Thr, Ile,
; OTHER INFORMATION: Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, a stop codon,
; OTHER INFORMATION: Tyr, Trp, Cys, or Phe.
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (36)..(36)
; OTHER INFORMATION: The 'Xaa' at location 36 stands for Lys, Glu, Gln, or a stop
; OTHER INFORMATION: codon.
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (40)..(40)
; OTHER INFORMATION: The 'Xaa' at location 40 stands for Lys, Asn, Arg, Ser, Thr, Ile,
; OTHER INFORMATION: Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, a stop codon,
; OTHER INFORMATION: Tyr, Trp, Cys, or Phe.
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (70)..(70)
; OTHER INFORMATION: The 'Xaa' at location 70 stands for Arg, or Ser.
; FEATURE:
```

NAME/KEY: misc_feature
 LOCATION: (71)..(71)
 OTHER INFORMATION: The 'Xaa' at location 71 stands for Glu, Gly, Ala, or Val.
 FEATURE:
 NAME/KEY: misc_feature
 LOCATION: (72)..(72)
 OTHER INFORMATION: The 'Xaa' at location 72 stands for Glu, Gly, Ala, or Val.
 FEATURE:
 NAME/KEY: misc_feature
 LOCATION: (103)..(103)
 OTHER INFORMATION: The 'Xaa' at location 103 stands for Lys, Asn, Arg, Ser, Thr,
 OTHER INFORMATION: Ile, Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, a stop
 OTHER INFORMATION: codon, Tyr, Trp, Cys, or Phe.
 FEATURE:
 NAME/KEY: misc_feature
 LOCATION: (105)..(105)
 OTHER INFORMATION: The 'Xaa' at location 105 stands for Asn, Asp, His, or Tyr.
 FEATURE:
 NAME/KEY: misc_feature
 LOCATION: (108)..(108)
 OTHER INFORMATION: The 'Xaa' at location 108 stands for Ile, or Phe.
 FEATURE:
 NAME/KEY: misc_feature
 LOCATION: (116)..(116)
 OTHER INFORMATION: The 'Xaa' at location 116 stands for Asn, Ser, Thr, or Ile.
 FEATURE:
 NAME/KEY: misc_feature
 LOCATION: (118)..(118)
 OTHER INFORMATION: The 'Xaa' at location 118 stands for a stop codon, Ser, or Leu.
 FEATURE:
 NAME/KEY: misc_feature
 LOCATION: (124)..(124)
 OTHER INFORMATION: The 'Xaa' at location 124 stands for Arg, Gly, or Trp.
 FEATURE:
 NAME/KEY: misc_feature
 LOCATION: (125)..(125)
 OTHER INFORMATION: The 'Xaa' at location 125 stands for Ile, Val, Leu, or Phe.
 FEATURE:
 NAME/KEY: misc_feature
 LOCATION: (130)..(130)
 OTHER INFORMATION: The 'Xaa' at location 130 stands for Arg, or Ser.
 FEATURE:
 NAME/KEY: misc_feature
 LOCATION: (135)..(135)
 OTHER INFORMATION: The 'Xaa' at location 135 stands for Asp, Gly, Ala, or Val.
 FEATURE:
 NAME/KEY: misc_feature
 LOCATION: (137)..(137)
 OTHER INFORMATION: The 'Xaa' at location 137 stands for Tyr, Cys, Ser, or Phe.
 FEATURE:
 NAME/KEY: misc_feature
 LOCATION: (142)..(142)
 OTHER INFORMATION: The 'Xaa' at location 142 stands for Thr, Ala, Pro, or Ser.
 FEATURE:
 NAME/KEY: misc_feature
 LOCATION: (147)..(147)
 OTHER INFORMATION: The 'Xaa' at location 147 stands for Leu, or Phe.
 FEATURE:
 NAME/KEY: misc_feature
 LOCATION: (155)..(155)
 OTHER INFORMATION: The 'Xaa' at location 155 stands for Asn, Ser, Thr, or Ile.
 FEATURE:
 NAME/KEY: misc_feature
 LOCATION: (159)..(159)
 OTHER INFORMATION: The 'Xaa' at location 159 stands for Lys, Arg, Thr, or Met.
 NAME/KEY: misc_feature
 LOCATION: (160)..(160)
 OTHER INFORMATION: The 'Xaa' at location 160 stands for Lys, Glu, Gln, or a
 OTHER INFORMATION: stop codon.
 US-10-267-849A-10

Query Match

54.2%, Score 26, DB 6, Length 163,

Best Local Similarity 66.7%; Pred. No. 88;
 Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 Oy 2 DAPGY 7
 Db 1 DSPAGY 6

Search completed: December 3, 2005, 23:29:23
 Job time : 7 secs